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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:16:16 ; Search time 22 Seconds  
(without alignments)  
492.793 Million cell updates/sec

Title: US-10-029-079-3  
Perfect score: 1166  
Sequence: 1 MKENVASATVFTLLFLNTCLNGQLPGCKPEIFKCRSPNKETFTCWNRPGTDGGLPTNY 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/prodata/2/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/prodata/2/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/prodata/2/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/prodata/2/iaa/PCRUS.COMB.pep.\*  
6: /cgn2\_6/prodata/2/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1155.5	99.1	349	3	US-08-806-597A-14
2	1155.5	99.1	349	3	US-08-970-428A-14
3	1042.5	89.4	599	3	US-09-000-145-2
4	863.5	74.1	593	3	US-09-000-145-4
5	809.5	69.4	592	3	US-09-000-145-6
6	679	58.2	134	3	US-08-806-597A-8
7	679	58.2	134	3	US-08-970-428A-8
8	387	33.2	118	3	US-08-806-597A-4
9	387	33.2	118	3	US-08-970-428A-4
10	297	25.5	389	3	US-09-071-224-25
11	297	25.5	389	3	US-09-071-224-26
12	296	25.4	303	3	US-09-071-224-21
13	296	25.4	385	3	US-09-071-224-20
14	296	25.4	388	3	US-09-071-224-17
15	296	25.4	389	3	US-09-071-224-27
16	296	25.4	389	3	US-09-071-224-31
17	296	25.4	422	3	US-09-071-224-2
18	295	25.3	389	3	US-09-071-224-30
19	294	25.2	389	3	US-09-071-224-28
20	294	25.2	389	3	US-09-071-224-24
21	294	25.2	389	3	US-09-071-224-29
22	293	25.1	303	3	US-09-071-224-23
23	293	25.1	389	3	US-09-071-224-22
24	293	25.1	392	3	US-09-071-224-18
25	293	25.1	422	4	US-08-866-028-32
26	293	25.1	425	3	US-09-071-224-4
27	292	25.0	385	3	US-09-071-224-19

28	292	25.0	405	3	US-09-012-072-2	Sequence 2, Appli
29	292	25.0	405	3	US-09-120-601-2	Sequence 2, Appli
30	292	25.0	425	3	US-09-071-224-6	Sequence 6, Appli
31	291.5	25.0	620	3	US-09-000-145-5	Sequence 5, Appli
32	289.5	24.8	620	3	US-09-000-145-3	Sequence 3, Appli
33	273	23.4	434	3	US-09-012-072-4	Sequence 4, Appli
34	273	23.4	434	3	US-09-120-601-4	Sequence 4, Appli
35	273	23.4	448	3	US-09-120-601-6	Sequence 6, Appli
36	262.5	22.5	620	3	US-09-000-145-1	Sequence 1, Appli
37	246	21.1	204	3	US-09-043-785-2	Sequence 2, Appli
38	237	20.3	48	3	US-08-806-597A-6	Sequence 6, Appli
39	237	20.3	48	3	US-08-970-428A-6	Sequence 6, Appli
40	227.5	19.5	148	1	US-08-224-982-3	Sequence 3, Appli
41	227.5	19.5	148	2	US-08-468-580-3	Sequence 3, Appli
42	227.5	19.5	148	3	US-08-643-212-2	Sequence 2, Appli
43	227.5	19.5	148	5	PCT-US95-03731-3	Sequence 3, Appli
44	223.5	19.2	148	1	US-08-224-982-4	Sequence 4, Appli
45	223.5	19.2	148	2	US-08-468-580-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-08-806-597A-14  
; Sequence 14, Application US/08806597A  
; Patent No. 6083714  
; GENERAL INFORMATION:  
; APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
; TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/806,597A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/012,503  
; FILING DATE: 29 February 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: KELLY=1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 349 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-806-597A-14

SEQ  
A.A.-25-349 - 14

Query Match 99.1%; Score 1155.5; DB 3; Length 349;  
Best Local Similarity 99.5%; Pred. No. 1.8e-116;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLNGQLPGCKPEIFKCRSPNKETFTCWNRPGTDGGLPTNY 60  
DB 1 MKENVASATVFTLLFLNTCLNGQLPGCKPEIFKCRSPNKETFTCWNRPGTDGGLPTNY 60

QY 61 SLTYHREGTLMHRCPDYITGGPNCHFGKQYTSMMRTYIMVNAT-QMGSSFSDELVD 119  
 Db 61 SLTYHREGTLMHRCPDYITGGPNCHFGKQYTSMMRTYIMVNAT-QMGSSFSDELVD 120  
 QY 120 VTYIVQDPPLLEAVEVKQEDRKPYLWIKWSPTLIDKTGWFTLLYEIRLKPAAEW 179  
 Db 121 VTYIVQDPPLLEAVEVKQEDRKPYLWIKWSPTLIDKTGWFTLLYEIRLKPAAEW 180  
 QY 180 EHFAGQOTFEKILSLHFGQKYLQVRCCKPD 210  
 Db 181 EHFAGQOTFEKILSLHFGQKYLQVRCCKPD 211

## RESULT 2

US-08-970-428A-14  
 ; Sequence 14, Application US/08970428A  
 ; Patent No. 6083753  
 ; GENERAL INFORMATION:  
 ; APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
 ; TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/970,428A  
 ; FILING DATE: 14-NOV-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/012,503  
 ; FILING DATE: 29-FEB-1996  
 ; PRIOR APPLICATION DATA: US 08/806,597  
 ; FILING DATE: 26-FEB-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: YUN, Allen C.  
 ; REGISTRATION NUMBER: 37,971  
 ; REFERENCE/DOCKET NUMBER: KELLY=1B  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 349 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Protein

US-08-970-428A-14

A.A. 25-349 - SEQ # 14

Query Match 99.1%; Score 1155.5; DB 3; Length 349;  
 Best Local Similarity 99.5%; Pred. No. 1.8e-116;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNCLNGQLPPGKPIFKCRSPNKETFTCWRRPGTGGGLPNY 60  
 Db 1 MKENVASATVFTLLFLNCLNGQLPPGKPIFKCRSPNKETFTCWRRPGTGGGLPNY 60  
 QY 61 SLTYHREGTLMHRCPDYITGGPNCHFGKQYTSMMRTYIMVNAT-QMGSSFSDELVD 119  
 Db 61 SLTYHREGTLMHRCPDYITGGPNCHFGKQYTSMMRTYIMVNAT-QMGSSFSDELVD 120  
 QY 120 VTYIVQDPPLLEAVEVKQEDRKPYLWIKWSPTLIDKTGWFTLLYEIRLKPAAEW 179  
 Db 121 VTYIVQDPPLLEAVEVKQEDRKPYLWIKWSPTLIDKTGWFTLLYEIRLKPAAEW 180

QY 180 EHFAGQOTFEKILSLHFGQKYLQVRCCKPD 210  
 Db 181 EHFAGQOTFEKILSLHFGQKYLQVRCCKPD 211

## RESULT 3

US-09-000-145-2  
 ; Sequence 2, Application US/09000145  
 ; Patent No. 6169172  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DEVAUCHELLE, Gerrard  
 ; APPLICANT: GARNIER, Laurence  
 ; APPLICANT: CAHOREAU, Claire  
 ; APPLICANT: CERUTTI, Martine  
 ; TITLE OF INVENTION: INTRACYTOPLASMIC DOMAIN FOR ACHIEVING PROTEIN SECRETION  
 ; FILE REFERENCE: 0384-0047-OXPECT  
 ; CURRENT APPLICATION NUMBER: US/09/000,145  
 ; CURRENT FILING DATE: 1998-03-16  
 ; EARLIER APPLICATION NUMBER: PCT/FR96/01237  
 ; EARLIER FILING DATE: 1996-08-02  
 ; EARLIER APPLICATION NUMBER: FR 95/09420  
 ; EARLIER FILING DATE: 1995-08-02  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 599  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-000-145-2

Query Match 89.4%; Score 1042.5; DB 3; Length 599;

Best Local Similarity 99.5%; Pred. No. 6.1e-104;  
 Matches 187; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 24 GQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNYSLTYHREGTLMHRCPDYITGGP 83  
 Db 1 GQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNYSLTYHREGTLMHRCPDYITGGP 60  
 QY 84 NSCHFGKQYTSMMRTYIMVNAT-QMGSSFSDELVDVTVIVQDPPLLEAVEVKQEDR 142  
 Db 61 NSCHFGKQYTSMMRTYIMVNAT-QMGSSFSDELVDVTVIVQDPPLLEAVEVKQEDR 120  
 QY 143 KPYLWIKWSPTLIDKTGWFTLLYEIRLKPAAEWIHFAGQOTFEKILSLHFGQKYL 202  
 Db 121 KPYLWIKWSPTLIDKTGWFTLLYEIRLKPAAEWIHFAGQOTFEKILSLHFGQKYL 180  
 QY 203 VQVRCKPD 210  
 Db 181 VQVRCKPD 188

## RESULT 4

US-09-000-145-4  
 ; Sequence 4, Application US/09000145  
 ; Patent No. 6169172  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DEVAUCHELLE, Gerrard  
 ; APPLICANT: GARNIER, Laurence  
 ; APPLICANT: CAHOREAU, Claire  
 ; APPLICANT: CERUTTI, Martine  
 ; TITLE OF INVENTION: USE OF A PROLACTIN RECEPTOR OR GROWTH HORMONE RECEPTOR  
 ; FILE REFERENCE: 0384-0047-OXPECT  
 ; CURRENT APPLICATION NUMBER: US/09/000,145  
 ; CURRENT FILING DATE: 1998-03-16  
 ; EARLIER APPLICATION NUMBER: PCT/FR96/01237  
 ; EARLIER FILING DATE: 1996-08-02  
 ; EARLIER APPLICATION NUMBER: FR 95/09420  
 ; EARLIER FILING DATE: 1995-08-02  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 4

; LENGTH: 593  
; TYPE: PRT  
; ORGANISM: Oryctolagus cuniculus  
US-09-000-145-4  
  
Query Match 74.1%; Score 863.5; DB 3; Length 593;  
Best Local Similarity 79.3%; Pred. No. 1.3e-84;  
Matches 149; Conservative 19; Mismatches 20; Indels 1; Gaps 1;  
  
QY 24 GQLPPGKPIFKCRSPNKTFTCWMPGTDGGLPTNYSLYTHREGETLMHECPDYITGSP 83  
Db 1 GQSPGKPIFKCRSPNKTFTCWMPGADGGLPTNYSLYTHREGETLMHECPDYITGSP 60  
  
QY 84 NSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELVDVTVIVQPPLELAVEVKQPEDR 142  
Db 61 NSCYFSEKTSITWIIITVATNQMSSVSDRYVDVTVIVQPPLELAVEVKQPEDR 120  
  
QY 143 KPYLWKWSPPTLIDLTGNTLLYIRLKPKEAEWEIHFAGQQTFFKILSLHPGQKYL 202  
Db 121 KPYLWKWSPPTLIDVRSGLTLLQYIRLKPKEAEWEIHFAGQQTFFKILSLHPGQKYL 180  
  
QY 203 VQVRCKPD 210  
Db 181 VQVRCKPD 188

RESULT 5  
US-09-000-145-6  
; Sequence 6, Application US/09000145  
; Patent No. 6169172  
; GENERAL INFORMATION:  
; APPLICANT: DEVAUCHELLE, Gerard  
; APPLICANT: GARNIER, Laurence  
; APPLICANT: CAHOREAU, Claire  
; APPLICANT: CERUTTI, Martine  
; TITLE OF INVENTION: USE OF A PROLACTIN RECEPTOR OR GROWTH HORMONE RECEPTOR  
; FILE OF INVENTION: INTRACYTOPLASMIC DOMAIN FOR ACHIEVING PROTEIN SECRETION  
; FILE REFERENCE: 0384-0047-0XPCT  
; CURRENT APPLICATION NUMBER: US/09/000,145  
; CURRENT FILING DATE: 1998-03-16  
; EARLIER APPLICATION NUMBER: PCT/FR96/01237  
; EARLIER FILING DATE: 1996-08-02  
; EARLIER APPLICATION NUMBER: FR 95/09420  
; EARLIER FILING DATE: 1995-08-02  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
US-09-000-145-6

Query Match 69.4%; Score 809.5; DB 3; Length 592;  
Best Local Similarity 74.5%; Pred. No. 8.7e-79;  
Matches 140; Conservative 19; Mismatches 28; Indels 1; Gaps 1;  
  
QY 24 GQLPPGKPIFKCRSPNKTFTCWMPGTDGGLPTNYSLYTHREGETLMHECPDYITGSP 83  
Db 1 GQSPGKPIFKCRSPNKTFTCWMPGADGGLPTNYSLYTHREGETLMHECPDYITGSP 60  
  
QY 84 NSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELVDVTVIVQPPLELAVEVKQPEDR 142  
Db 61 NSCYFSEKTSITWIIITVATNQMSSVSDRYVDVTVIVQPPLELAVEVKQPEDR 120  
  
QY 143 KPYLWKWSPPTLIDLTGNTLLYIRLKPKEAEWEIHFAGQQTFFKILSLHPGQKYL 202  
Db 121 KPYLWKWSPPTLIDVRSGLTLLQYIRLKPKEAEWEIHFAGQQTFFKILSLHPGQKYL 180  
  
QY 203 VQVRCKPD 210  
Db 181 VQVRCKPD 188

RESULT 6  
US-08-806-597A-8  
; Sequence 8, Application US/08806597A  
; Patent No. 6083714  
; GENERAL INFORMATION:  
; APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
; TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/806,597A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/012,503  
; FILING DATE: 29 February 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: KELLY-1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 134 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-806-597A-8

Query Match 58.2%; Score 679; DB 3; Length 134;  
Best Local Similarity 96.9%; Pred. No. 1.4e-65;  
Matches 125; Conservative 0; Mismatches 0; Indels 4; Gaps 2;  
  
QY 1 MKNVASATVFTLLFLNTCLLNGQLPGKPEIFKCRSPNKTFTCWMPGTDGGLPTNY 60  
Db 1 MKNVASATVFTLLFLNTCLLNGQLPGKPEIFKCRSPNKTFTCWMPGTDGGLPTNY 60  
  
QY 61 SLTYHREGETLMHECPDYITGPNPSCHFGKQYTSWRTYIMVNAT-CMGSSFSDELVD 119  
Db 61 SLTYHREGETLMHECPDYITGPNPSCHFGKQYTSWRTYIMVNAT-CMGSSFSDELVD 120  
  
QY 120 VTYIVQDPD 128  
Db 121 VTYIVQDPD 126

RESULT 7  
US-08-970-428A-8  
; Sequence 8, Application US/08970428A  
; Patent No. 6083753  
; GENERAL INFORMATION:  
; APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
; TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA

ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/970,428A  
 FILING DATE: 14-NOV-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/012,503  
 FILING DATE: 29-FEB-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/806,597  
 FILING DATE: 26-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: YUN, Allen C.  
 REGISTRATION NUMBER: 37,971  
 REFERENCE/DOCKET NUMBER: KELLY=1B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 134 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-970-428A-8

Query Match 58.2%; Score 679; DB 3; Length 134;  
 Best Local Similarity 96.9%; Pred. No. 1.4e-65;  
 Matches 125; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 DB 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 QY 61 SLTYHREGELTMECPDYITGGPNSCHFGKQYTSMTWRTYIMVNAT-QNGSSFSDELXYD 119  
 DB 61 SLTYHREGELTMECPDYITGGPNSCHFGKQYTSMTWRTYIMVNATQNGSSFSDELXYD 120  
 QY 120 VTYVQDPD 128  
 DB 121 VTYV---DP 126

RESULT 8  
 US-08-806-597A-4  
 Sequence 4, Application US/08806597A  
 Patent No. 6083714  
 GENERAL INFORMATION:  
 APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
 TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/806,597A  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/012,503

FILING DATE: 29 February 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: KELLY=1A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 118 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-806-597A-4

Query Match 33.2%; Score 387; DB 3; Length 118;  
 Best Local Similarity 95.8%; Pred. No. 3.8e-34;  
 Matches 69; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 DB 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 QY 61 SLTYHREGELTLM 72  
 DB 61 SLTYHREGSILL 72

RESULT 9  
 US-08-970-428A-4  
 Sequence 4, Application US/08970428A  
 Patent No. 6083753  
 GENERAL INFORMATION:  
 APPLICANT: KELLY, Paul A. and NAGANO, Makoto  
 TITLE OF INVENTION: SOLUBLE HUMAN PROLACTIN RECEPTORS  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/970,428A  
 FILING DATE: 14-NOV-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/012,503  
 FILING DATE: 29-FEB-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/806,597  
 FILING DATE: 26-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: YUN, Allen C.  
 REGISTRATION NUMBER: 37,971  
 REFERENCE/DOCKET NUMBER: KELLY=1B  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 118 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-970-428A-4





```

132 QY LAV-EVKQEDBRKPYLWIKWSPPTLIDUKTGWFTLLYEIRLKPEKAAEW- IHFAQQOTE 189
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
204 Db VHSRVGGLEDQLSVRWV--SPPALKDF--LFQAKYQIRYVEDSDWMKVVDVSNQTS 258
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
190 QY FKILSLHPGQKYLVQVRCKP 209
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
259 Db CRLAGLKPCTVYFVQVRNCP 278
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 12
US-09-071-224-21
/ Sequence 21, Application US/09071224
/ Patent No. 62711343
/ GENERAL INFORMATION:
/ APPLICANT: Lok, Si
/ APPLICANT: Presnell, Scott R.
/ APPLICANT: Jelmberg, Anna C.
/ APPLICANT: Gilbert, Teresa
/ APPLICANT: Foster, Donald C.
/ APPLICANT: Adams, Robyn L.
/ APPLICANT: Lehner, Joyce M.
/ TITLE OF INVENTION: MAMMALIAN ZCYTORS
/ NUMBER OF SEQUENCES: 37
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Zymogenetics
/ STREET: 1201 Eastlake Ave East
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/071,224
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lunn, Paul G
/ REGISTRATION NUMBER: 32,743
/ REFERENCE/DOCKET NUMBER: 96-22
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 206-442-6627
/ TELEFAX: 206-442-6678
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 303 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ JS-09-071-224-21

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Query Match	25.4%	Score 296;	DB 3;	Length 303;
Best Local Similarity	38.0%	Prod. No. 9.5e-24;		
Matches	76;	Conservative	27;	Mismatches 85; Indels 12; Gaps 8;
aa	15	LFNTCLLNQLPQPKGFPEIKFCRSPNKEFTTCWRPGTDGG-	LFNTNSLYAHREGETLM	72
bb	86	ILAGSCLYVG-LPEPEVNVISCSWKMKDLTCRTFPGAHGETFLTNSLYKLRWYQD	144	
aa	73	HECPDITGGPNSCHFGKQYTSWRTYIMNNAT-QMGSSFSDELYVDVTYVDPDPPLE	131	
bb	145	NTCEEYHTVGPHSCHIPKO-LALFTSYEIMWEATNRLGARSVDVLTLDILDVVTVDTPPE	203	
aa	132	LAV-EVKQPEDRKPYLWIKWSPPPTLDLTGTFYLYEIRLKPKEKAASWE-IHEFAGQOTE	189	

```

Db      204 VHVSRVGGLEDQLSVRWV--SPPALKDF---LFOAKYQIRYRVEDSYDMWKVDCVSNQTS 258
Qy      190 FKILSLHPGQKYLQVRCRK 209
      :: ||| |||||
Db      259 CRLAGLKPGTVYFVQVRCNP 278

RESULT 13
US-09-071-224-20
; Sequence 20, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmsberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MANUAIAN ZCYTOR5
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-224-20

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	Query Match	25.4*	Score 296;	DB 3;	Length 385;
	Best Local Similarity	38.0%;	Prod. No. 1.3e-23;		
	Matches	76;	Conservative	27;	Mismatches 85; Indels 12; Gaps 8;
QY	15	LFLNTCLLNGQLPGKGEIFKCBSPNKEFTTCWAPGTDGG--LPTNYSLYIYHREGETLM	72		
Db	86	ILAGSCLYVG-LPPEKPVNISCWSRNMKDLTCRWTFPGAHGETFLHTNYSLYKRYKLEWYQGD	144		
QY	73	HECPDYITGGPNSCHFCKQYTSWRTYIMNNAT--QMGSSFSDELYVDVTVIVQPDPELE	131		
Db	145	NTCEEYHTVGHPSCHIPKD-LALFPYELIWEATNRLGSAESDVLTLDLVDVTTDDPPE	203		
QY	132	LAV-EVVKQPEDRPXYIWKNSPPTLIDLKTGFTLLYLIRLKPKEAAEWE-IHFAGQOTE	189		
Db	204	VHYSRVGGLEDQLSVRMV--SPPALKDF---LFOAKYQIRYRVSDSVDMKVVDDVSQOTS	258		

QY 190 FKILSLHPGQKYLQVRCCKP 209  
Db 259 CRLAGLKPQTVYFVQVRCNP 278

RESULT 14  
US-09-071-224-17  
; Sequence 17, Application US/09071224  
; Patent No. 6271343  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zymogenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,224  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 388 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-071-224-17

Query Match 25.4%; Score 296; DB 3; Length 388;  
Best Local Similarity 38.0%; Pred. No. 1.3e-23;  
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;  
QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTYYHREGETLM 72  
Db 89 ILAGSLYVG-LPPEKPNISCSWKNKDLTCRWTPGAHGETFLHTNYSKYKLRWYQD 147  
QY 73 HECPDYITGGNSCHFGKQYTSNWRTYIMVNAT-OMGSSFSDELYVDVTYIVQDPDPLE 131  
Db 148 NTCSEYHTVGPCHSHPKD-LALFTPEIWEATNRLGSRSDVLTLDLDVVTDDPPPE 206  
QY 132 LAV-EVKQPEDRKPYLWIKWSPTLTLKGTGFTLLYELRLKPKAAWE-IHFAGQOTE 189  
Db 207 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVEDSVDMKVVDDVSNQTS 261  
QY 190 FKILSLHPGQKYLQVRCCKP 209

Db 262 CRLAGLKPQTVYFVQVRCNP 281

RESULT 15  
US-09-071-224-27  
; Sequence 27, Application US/09071224  
; Patent No. 6271343  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Jelmsberg, Anna C.  
; APPLICANT: Gilbert, Teresa  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Adams, Robyn L.  
; APPLICANT: Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zymogenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,224  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 389 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-071-224-27

Query Match 25.4%; Score 296; DB 3; Length 389;  
Best Local Similarity 38.0%; Pred. No. 1.3e-23;  
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;  
QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTYYHREGETLM 72  
Db 86 ILAGSLYVG-LPPEKPNISCSWKNKDLTCRWTPGAHGETFLHTNYSKYKLRWYQD 144  
QY 73 HECPDYITGGNSCHFGKQYTSNWRTYIMVNAT-OMGSSFSDELYVDVTYIVQDPDPLE 131  
Db 145 NTCSEYHTVGPCHSHPKD-LALFTPEIWEATNRLGSRSDVLTLDLDVVTDDPPPD 203  
QY 132 LAV-EVKQPEDRKPYLWIKWSPTLTLKGTGFTLLYELRLKPKAAWE-IHFAGQOTE 189  
Db 204 VHVSRVGGLEDQLSVRWV--SPALKDF--LFOAKYQIRYRVEDSVDMKVVDDVSNQTS 258  
QY 190 FKILSLHPGQKYLQVRCCKP 209  
Db 259 CRLAGLKPQTVYFVQVRCNP 278

Thu May 13 08:55:52 2004

us-10-029-079-3.ra1

Page 8

Search completed: May 12, 2004, 16:20:03  
Job time : 23 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:10:55 ; Search time 61 Seconds  
(without alignments)  
972.705 Million cell updates/sec

Title: US-10-029-079-3  
Perfect score: 1166  
Sequence: 1 MKNVASATVFTLLFLNTC.....KILSLHPGKYLQVRCKPD 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1166	100.0	210	5	ABG70827 Human rec
2	1155.5	99.1	349	3	AAy96921 Soluble h
3	1155.5	99.1	349	3	AAy95527 Human pro
4	1155.5	99.1	622	2	AAr10795 Human pro
5	1155.5	99.1	622	5	ABj05555 Breast ca
6	1155.5	99.1	622	5	AAu99354 Human pro
7	1155.5	99.1	622	6	ABr47567 Breast ca
8	1154.5	99.0	622	5	AAu99355 Human pro
9	1036.5	88.9	211	2	AAr24273 Truncated
10	1036.5	88.9	211	2	AAr22228 Truncated
11	987	84.6	597	7	AAE28697 Human NOV
12	679	58.2	134	3	AAy96918 Soluble h
13	679	58.2	134	3	AAy95526 Soluble i
14	549.5	47.1	606	2	AAr93121 Tilapia p
15	549.5	47.1	630	2	AAr93120 Tilapia p
16	387	33.2	118	3	AAy96916 Soluble h
17	387	33.2	118	3	AAy95524 Soluble i
18	297	25.5	389	2	AAW70847 Human zcy
19	297	25.5	389	2	AAW70848 Human zcy
20	296	25.4	303	2	AAW70843 Human zcy
21	296	25.4	385	2	AAW70842 Human zcy
22	296	25.4	388	2	AAW70839 Human zcy
23	296	25.4	389	2	AAW70849 Human zcy
24	296	25.4	389	2	AAW70853 Human zcy
25	296	25.4	422	2	AAW70860 Human zcy

26	295	25.3	183	2	AAr25244 Truncated
27	295	25.3	389	2	AAW70852 Human zcy
28	294	25.2	389	2	AAW70851 Human zcy
29	294	25.2	389	2	AAW70846 Human zcy
30	294	25.2	389	2	AAW70850 Human zcy
31	293	25.1	303	2	AAW70845 Human zcy
32	293	25.1	350	2	AAW55015 Amino aci
33	293	25.1	350	4	AAE00824 Human NR6
34	293	25.1	389	2	AAW70844 Human zcy
35	293	25.1	392	2	AAW70840 Human zcy
36	293	25.1	408	2	AAW59805 Amino aci
37	293	25.1	408	2	AAy26338 Human U4
38	293	25.1	410	2	AAy29779 Human DNA
39	293	25.1	410	3	ABi19588 Human cyt
40	293	25.1	410	4	AB36647 Human cyt
41	293	25.1	410	7	ADC07179 Human cyt
42	293	25.1	421	4	AAE00826 Murine ha
43	293	25.1	422	2	AAy05782 Human typ
44	293	25.1	422	2	AAy06479 Human tum
45	293	25.1	422	2	AAy17825 Human PRO

ALIGNMENTS

RESULT 1

ABG70827  
ID ABG70827 standard; protein; 210 AA.  
XX  
AC ABG70827;  
XX  
DT 17-DEC-2002 (first entry)  
XX  
DE Human recombinant prolactin-binding protein, rhPRLBP.  
XX  
KW Human; prolactin-binding protein; PRLBP; prolactin receptor; PRLR;  
KW growth hormone receptor; GHR; transmembrane protein; hormone; prolactin;  
KW PRL; growth hormone; GH; homodimerisation; receptor-associated kinase;  
KW signalling cascade; rhPRLBP; recombinant hPRLBP; extracellular domain;  
KW ECD; cancer; Nb2; cellular proliferation; diagnosis; somatolactogenic;  
KW pituitary adenoma; hyperprolactinaemia; gigantism; acromegaly;  
KW osteopathic.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 106..107  
FT /note= "Encoded by ACTAACCAG"

XX US2002119154-A1.

XX 29-AUG-2002.

XX 21-DEC-2001; 2001US-00029079.

XX 22-DEC-2000; 2000US-0258285P.

(CLEV/) CLEVANGER C V.

(KLIN/) KLINE J B.

Clevanger CV, Kline JB;

WPI; 2002-750044/81.

DR N-PSDB; ABS55241.

PT Novel human prolactin-binding protein, useful for modulating  
somatolactogenic function and for inhibiting Nb2 cells in animals.

XX Disclosure; Page 6; 13pp; English.

XX The invention discloses a human prolactin-binding protein (PRLBP). Both  
CC the prolactin receptor (PRLR) and the growth hormone receptor (GHR) are  
CC single chain transmembrane proteins. The hormones prolactin (PRL) and



```

XX PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX PI Kelly PA, Nagano M;
XX DR WPI; 2000-464346/40.
XX DR N-PSDB; AAA49980.
XX PT New recombinant DNA having a segment encoding a signal peptide joined
XX PT translationally to a segment encoding a soluble human prolactin receptor
XX PT useful as a hormone growth hormone binding protein, and in x-ray
XX PT crystallographic analysis.
XX PS Claim 15; Col 35-38; 27pp; English.
XX CC The present sequence is that of a newly identified isoform of the human
XX CC prolactin receptor (PRLR), which lacks a large part of the intracellular
XX CC domain (amino acids 312-503) of the full-length receptor and has a short
XX CC cytoplasmic tail. 6 isoforms (see AAA49976-82) of human PRLR have been
XX CC identified in human colonic Caco-2 and human breast cancer T-47D cells.
XX CC Recombinant DNA molecules encoding the soluble PRLR proteins are
XX CC provided, as well as expression vectors and host cells. The soluble PRLRs
XX CC may be used as binding proteins for human prolactin and/or human growth
XX CC hormone, which can be useful in diagnostics for the detection and
XX CC measurement of the binding ligand, or in therapeutics for binding to
XX CC human prolactin and/or human growth hormone to retard or inhibit their
XX CC hormone activities. They may also be used in place of monoclonal
XX CC antibodies to provide solution-based radioligand receptor assays, in
XX CC receptor sandwich or enzymatic assays, and in x-ray crystallographic
XX CC analysis to develop molecular models that define the tertiary structure
XX CC of the hormone-binding domains, where such information would provide
XX CC insight into the structure of the actual contact between a hormone and
XX CC its receptor. This structural information would be useful in the design
XX CC of peptides that have prolactin or growth hormone-like agonistic or
XX CC antagonistic activity
XX SQ Sequence 349 AA;
    Query Match          99.1%; Score 1155.5; DB 3; Length 349;
    Best Local Similarity 99.5%; Pred. No. 1.4e-105;
    Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMNVAT-CMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMNVATNMQSGSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFGAQQTFFKILSLHFGQKYLQVRCRCPD 210
DB 181 EIHFGAQQTFFKILSLHFGQKYLQVRCRCPD 211
RESULT 4
ID AAR10795 standard; protein; 622 AA.
XX AC AAR10795;
XX DT 25-APR-1991 (first entry)
XX DE Human prolactin receptor.
XX KW Human prolactin receptor; PRL; assay; antibody; growth hormone.
XX OS Homo sapiens.

```

```

XX FH Key Location/Qualifiers
XX FT Peptide 1..24
XX FT /label= sig_peptide
XX FT Protein 25..622
XX FT /label= mat_protein
XX PN US4992378-A.
XX PD 12-FEB-1991.
XX PF 16-DEC-1988; 88US-00286445.
XX PR 16-DEC-1988; 88US-00286445.
XX PA (ROYA-) ROYAL INST ADVAN LE.
XX PI Kelly PA, Djiane J;
XX WPI; 1991-065341/09.
XX N-PSDB; AAQ10550.
XX Isolated cDNA sequence encoding human prolactin receptor - useful for
XX expressing the receptor, e.g. for screening assays and antibody prodn.
XX Disclosure; Fig 1 (A-E); 11pp; English.
XX The human PRL receptor cDNA is isolated by screening a lambda gt 10
XX library prepared from normal human hepatoma Hep G2 and T47-D breast
XX cancer cells. Initially, 1x106 recombinants are screened with the
XX following probe: a complementary RNA of the F3 cDNA of the rat prolactin
XX receptor. One positive recombinant was isolated from the Hep G2 library;
XX cDNA was later used as a probe to rescreen the library. Five additional
XX cDNAs were identified, and by combining two of the six cDNAs, a PRL
XX receptor cDNA of 2.5 kb was constructed, contg. a single ORF of 1866 bp.
XX Similar partial length cDNA were isolated from the T47-D library. Several
XX regions of sequence identity between the human growth hormone and PRL
XX receptors can be found, both in the extracellular and cytoplasmic
XX domains. The sequence is an important genetic engineering tool which may
XX be used for the screening of growth hormone variants, for the development
XX of test kits to measure PRL receptor levels in human breast and prostate
XX cancer biopsies, for the measurement of bioactive forms of prolactin,
XX and for the development of drugs to induce stimulation or inhibition of
XX the immune system
XX SQ Sequence 622 AA;
    Query Match          99.1%; Score 1155.5; DB 2; Length 622;
    Best Local Similarity 99.5%; Pred. No. 2.9e-105;
    Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMNVAT-CMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMNVATNMQSGSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVQKPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFGAQQTFFKILSLHFGQKYLQVRCRCPD 210
DB 181 EIHFGAQQTFFKILSLHFGQKYLQVRCRCPD 211
RESULT 5
ID ABJ05555 standard; protein; 622 AA.
XX AC ABJ05555;

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XX DT 14-NOV-2002 (first entry)  
XX DE Breast cancer-associated protein 20.  
XX KW Breast cancer; breast cancer-associated gene sequence; drug development;  
XX OS pharmacogenetics; biosensor development.  
XX XX Unidentified.  
XX PN WO200259377-A2.  
XX PD 01-AUG-2002.  
XX XX 24-JAN-2002; 2002WO-US002242.  
XX PF 24-FEB-2001; 2001US-0263965P.  
XX PR 02-FEB-2001; 2001US-0265928P.  
XX PR 09-APR-2001; 2001US-00829472.  
XX PR 09-APR-2001; 2001US-0282698P.  
XX PR 04-MAY-2001; 2001US-0288590P.  
XX PR 29-MAY-2001; 2001US-0294443P.  
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX XX Mack DH, Gish KC, Afar D;  
XX XX WPI; 2002-583738/62.  
XX DR N-PSDB; ABT07712.  
XX XX Detecting a breast cancer-associated transcript in a patient's cell.  
XX PT useful for diagnosing breast cancer, comprises contacting a biological  
XX PT sample with a polynucleotide that selectively hybridizes with breast  
XX PT cancer nucleic acids.  
XX XX Disclosure; Page 365; 414pp; English.  
XX PS The invention comprises a method of detecting a breast cancer-associated  
XX CC transcript in a cell from a patient. The method of the invention involves  
XX CC contacting a biological sample from the patient with a nucleotide that  
XX CC hybridizes to one of the 69 breast cancer-associated gene sequences shown  
XX CC in the specification. The method of the invention is useful in the  
XX CC diagnosis or prognosis of breast cancer, and for detecting genes that are  
XX CC up or down-regulated in breast cancer cells. Genes identified by the  
XX CC method of the invention can be used in diagnostic purposes and also as  
XX CC targets for screening for therapeutic compounds that modulate breast  
XX CC cancer (e.g. hormones or antibodies). Identification of genes that are  
XX CC over or under expressed in breast cancer can additionally provide high-  
XX CC resolution, high-sensitivity datasets which can be used in the areas of  
XX CC diagnostics, therapeutics, drug development, pharmacogenetics, protein  
XX CC structure and biosensor development. Amino acid sequences ABJ05536 -  
XX CC ABJ05604 represent the proteins encoded by the 69 breast cancer-  
XX CC associated genes of the invention  
XX XX Sequence 622 AA;  
XX XX Query Match 99.1%; Score 1155.5; DB 5; Length 622;  
XX XX Best Local Similarity 99.5%; Pred. No. 2.9e-105;  
XX XX Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MKENVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
DB 1 MKENVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
QY 61 SLTYHREGTLMHECPDYITGPNCHFGKQVTSWRTYIMVNAT-QVGSFSFSDLYVD 119  
DB 61 SLTYHREGTLMHECPDYITGPNCHFGKQVTSWRTYIMVNATNQVGSFSFSDLYVD 120  
QY 120 VYIYVQDPDPLELAVVEKQEDRKPYLWIKWSPFLIDLKTGFWTLLYEIRLKPKEAEW 179  
DB 121 VYIYVQDPDPLELAVVEKQEDRKPYLWIKWSPFLIDLKTGFWTLLYEIRLKPKEAEW 180  
QY 180 EIHFAQQQTEFKILSLHPGQKYLQVRCKPD 210

DB 181 EIHFAQQQTEFKILSLHPGQKYLQVRCKPD 211  
RESULT 6  
AAU99354  
ID AAU99354 standard; protein; 622 AA.  
XX AC AAU99354;  
XX DT 07-OCT-2002 (first entry)  
XX XX Human prolactin receptor (PRLR) protein.  
XX DE Human prolactin receptor; PRLR; cytostatic; immunosuppressive;  
XX KW chromosome 5p14-p13; neuroendocrine hormone; prolactin; PRL;  
XX KW breast growth; breast differentiation; puberty; pregnancy; lactation;  
XX KW mammary disorder; breast cancer; autoimmune disease; hyperprolactinaemia;  
XX KW gene therapy.  
XX OS Homo sapiens.  
XX XX WO200250098-A2.  
XX PN 27-JUN-2002.  
XX PD 18-DEC-2001; 2001WO-US049049.  
XX PF 18-DEC-2000; 2000US-0256523P.  
XX PR (GENA-) GENAISSANCE PHARM INC.  
XX PA Bieglecki KM, Duda A, Koshy B;  
XX PI WPI; 2002-528446/56.  
XX DR N-PSDB; ABK87971.  
XX XX Novel genetic variants of Prolactin Receptor isogenes, useful for  
XX PT improving efficiency and reliability in drug development for treating  
XX PT breast cancer, autoimmune diseases and hyperprolactinemia.  
XX PS Claim 27; Fig 3; 81pp; English.  
XX CC The invention discloses an isolated polynucleotide and polypeptide of the  
XX CC human prolactin receptor (PRLR). The neuroendocrine hormone prolactin  
XX CC (PRL) stimulates breast growth and differentiation during puberty,  
XX CC pregnancy and lactation. PRL has been implicated in the etiology of  
XX CC mammary disorders, such as breast cancer, and since PRLR mediates the  
XX CC effects of prolactin, it may also be involved in the etiology of the  
XX CC disease. The polypeptides are useful in screening for drugs that are  
XX CC useful for treating breast cancer, autoimmune diseases,  
XX CC hyperprolactinaemia and diseases associated with PRLR activity. The  
XX CC haplotyping method is also used by the pharmaceutical research scientist  
XX CC to validate PRLR as a candidate target for treating these specific  
XX CC conditions or diseases predicted and in the design of clinical trials for  
XX CC treating a specific condition of disease associated with PRLR activity.  
XX CC Antibodies raised against PRLR are useful in diagnostic, prognostic and  
XX CC therapeutic methods. The polynucleotide is useful for gene therapy and in  
XX CC studying the expression and function of PRLR and the effect of the single  
XX CC nucleotide polymorphisms (SNP) on the biological activity of PRLR. The  
XX CC sequence presented is the human prolactin receptor (PRLR) protein which  
XX CC is encoded by the gene located on chromosome 5p.4-p13  
XX XX Sequence 622 AA;  
XX XX Query Match 99.1%; Score 1155.5; DB 5; Length 622;  
XX XX Best Local Similarity 99.5%; Pred. No. 2.9e-105;  
XX XX Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MKENVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
DB 1 MKENVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60



QY	61	SLTYHREGETLMHECPDVIITGGPNSCHFGKOYTSKWETYYIMVNAT-QMGSSFSDELVD	119
Db	61	SLTYHREGETLMHECPDVIITGGPNSCHFGKOYTSKWETYYIMVNATQMGSSFSDELVD	120
QY	120	VVYIVQPPPLELAVEVQPEDRPXYLWIKWSPPTLIDLTKGTFTLLYEIRLKPXAASW	179
Db	121	VVYIVQPPPLELAVEVQPEDRPXYLWIKWSPPTLIDLTKGTFTLLYEIRLKPXAASW	180
QY	180	ETIHFAQQOTEFKILSLHPGQKYLQVQRCKPD	210
Db	181	ETIHFAQQOTEFKILSLHPGQKYLQVQRCKPD	211
RESULT 7			
ABR47567	ID	ABR47567 standard; protein; 622 AA.	
XX	AC	ABR47567;	
XX	DT	12-JUN-2003 (first entry)	
XX	DE	Breast cancer associated protein sequence SEQ ID NO:373.	
XX	KW	Human; breast cancer; cytostatic; gene therapy.	
XX	OS	Homo sapiens.	
XX	PN	WO2003004989-A2.	
XX	XX	16-JAN-2003.	
XX	PD	21-JUN-2002; 2002WO-US019669.	
XX	PF	21-JUN-2001; 2001US-0299887P.	
PR	PR	27-JUN-2001; 2001US-0301572P.	
PR	PR	18-JUL-2001; 2001US-0306501P.	
PR	PR	25-SEP-2001; 2001US-0325002P.	
PR	PR	05-MAR-2002; 2002US-0362585P.	
PR	PR	14-MAY-2002; 2002US-0380391P.	
XX	XX	(WILL-) MILLENIUM PHARM INC.	
XX	PA	Lillie J, Gannavarapu M, Glatt K, Hoersh S, Kamatkar S;	
PI	PI	Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;	
PI	PI	Bast RC, Hortobagyi GN, Fuszta L, Meric F, Sahin A, Mills GB;	
XX	XX	WPI; 2003-210381/20.	
DR	DR	N-PSDB; ACC50366.	
DR	DR	Breast cancer diagnosis or treatment by comparing the level of expression	
PT	PT	of a marker in a patient sample with that in the control non-breast	
PT	PT	cancer sample.	
XX	XX	Claim 1; SEQ ID NO 373; 128pp; English.	
PS	PS	The present invention describes a method for assessing whether a patient	
XX	XX	is afflicted with breast cancer. The method comprises comparing the level	
CC	CC	of expression of a marker (gene/polypeptide see ACC50076 to ACC50334 and	
CC	CC	ABR47386 to ABR47632) in a patient sample and the normal level of	
CC	CC	expression of the marker in a control non-breast cancer sample, where a	
CC	CC	significant increase in the level of expression of the marker in the	
CC	CC	patient sample and the normal level is an indication that the patient is	
CC	CC	afflicted with breast cancer. The breast cancer associated sequences from	
CC	CC	the present invention have cytostatic activities and can be used in gene	
CC	CC	therapy. The method is useful for diagnosing and treating breast cancer.	
CC	CC	N.B. The sequence data for this patent did not form part of the printed	
CC	CC	specification, but was obtained in electronic format directly from WIPO	
CC	CC	at ftp.wipo.int/pub/published_pct_sequences	
XX	XX	Sequence 622 AA;	
XX	XX	Query Match 99.1%; Score 1155.5; DB 6; Length 622;	
XX	XX	Best Local Similarity 99.5%; Pred No. 2.9e-105;	

CC conditions or diseases predicted and in the design of clinical trials for  
CC treating a specific condition of disease associated with PRLR activity.  
CC Antibodies raised against PRLR are useful in diagnostic, prognostic and  
CC therapeutic methods. The polynucleotide is useful for gene therapy and in  
CC studying the expression and function of PRLR and the effect of the single  
CC nucleotide polymorphisms (SNP) on the biological activity of PRLR. The  
CC sequence presented is the human prolactin receptor (PRLR) protein,  
CC variant #2, which is encoded by the gene located on chromosome 5p14-p13.  
CC Note: This sequence is not shown in the specification but was created by  
CC the indexer from information given in figure 3

XX SQ Sequence 622 AA;

Query Match 99.0%; Score 1154.5; DB 5; Length 622;  
Best Local Similarity 99.1%; Pred. No. 3.6e-105;  
Matches 209; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGPKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60  
DB 1 MKNVASATVFTLLFLNTCLLNGQLPPGPKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60  
QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMTWRTYIMVNAT-QMGSSFSDELYVD 119  
DB 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMTWRTYIMVNATQMGSSFSDELYVD 120  
QY 120 VTYIVQDPPELEAVEVKQPEDRKPYLWIKWSPPTLIDLTGWTLLYELRLKPEKAAEW 179  
DB 121 VTYIVQDPPELEAVEVKQPEDRKPYLWIKWSPPTLIDLTGWTLLYELRLKPEKAAEW 180  
QY 180 EHFAGQTEFKILSLHPGOKYLVQVRCRPD 210  
DB 181 EHFAGQTEFKILSLHPGOKYLVQVRCRPD 211

## RESULT 9

AAR24273  
ID AAR24273 standard; protein; 211 AA.

XX AC AAR24273;

DT 20-JUL-1992 (first entry)

XX Truncated human prolactin binding protein variant.

XX hPRLbp; placental lactogen; zinc finger; chelate;  
KW receptor-ligand complex.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 188  
FT /note= "wild-type His replaced by Ala"

XX WO9203478-A.

XX 05-MAR-1992.

XX 16-AUG-1991; 91WO-US005856.

XX 17-AUG-1990; 90US-00568936.

XX (GETH ) GENENTECH INC.

XX Bass SH, Cunningham BC, Fuh G, Lowman HB, Matthews DJ, Wells JA;

XX WPI; 1992-096838/12.

XX New method of modifying polypeptide hormone-receptor complex - to produce  
PT human growth hormone variant, useful for stimulating lactogenic and  
PT somatogenic response.

XX Claim 41; Page 56; 74pp; English.

XX

CC Plasmid pHPRLbp(1-211) (see AAR22228) coding for truncated, soluble  
CC prolactin binding protein was mutagenised such that the His codon at  
CC position 188 was substituted by an Ala codon. The hPRLbp variant has  
CC altered binding affinity for hGH

XX SQ Sequence 211 AA;

Query Match 88.9%; Score 1036.5; DB 2; Length 211;  
Best Local Similarity 99.5%; Pred. No. 4.3e-94;  
Matches 186; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 25 QLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTVHREGETLMHECPDYITGGPN 84

DB 1 QLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTVHREGETLMHECPDYITGGPN 60

QY 85 SCHFGKQYTSMTWRTYIMVNAT-QMGSSFSDELYVDVTYIVQDPPELEAVEVKQPEDRK 143

DB 61 SCHFGKQYTSMTWRTYIMVNATQMGSSFSDELYVDVTYIVQDPPELEAVEVKQPEDRK 120

QY 144 PYLWIKWSPPTLIDLTGWTLLYELRLKPEKAAEWIHFAGQTEFKILSLHPGOKYLV 203

DB 121 PYLWIKWSPPTLIDLTGWTLLYELRLKPEKAAEWIHFAGQTEFKILSLHPGOKYLV 180

QY 204 QVRCCKPD 210

DB 181 QVRCCKPD 187

## RESULT 10

AAR22228  
ID AAR22228 standard; protein; 211 AA.

XX AC AAR22228;

DT 20-JUL-1992 (first entry)

XX Truncated human prolactin binding protein.

XX hPRLbp; placental lactogen; zinc finger; chelate;  
KW receptor-ligand complex.

XX Homo sapiens.

XX WO9203478-A.

XX 05-MAR-1992.

XX 16-AUG-1991; 91WO-US005856.

XX 17-AUG-1990; 90US-00568936.

XX (GETH ) GENENTECH INC.

XX Bass SH, Cunningham BC, Fuh G, Lowman HB, Matthews DJ, Wells JA;  
XX WPI; 1992-096838/12.

XX New method of modifying polypeptide hormone-receptor complex - to produce  
PT human growth hormone variant, useful for stimulating lactogenic and  
PT somatogenic response.

XX Disclosure; Page 41; 74pp; English.

XX This truncated human prolactin binding protein is encoded by the insert  
CC contained in plasmid pHPRLbp(1-211). The hPRLbp gene fragment is  
CC transcribed under the control of the alkaline phosphatase promoter and  
CC secreted into the host (E.coli) periplasm under the direction of the stII  
CC signal sequence. A stop codon and MluI restriction site were introduced  
CC after the threonine 211 codon which immediately precedes the  
CC transmembrane domain of the receptor. The plasmid was used as a template  
CC for site-directed mutagenesis to modify the metal-chelating centre of the  
CC protein. See e.g. AAR24273 for an example of a preferred variant

SQ	Sequence 211 AA;	
Query Match	88.9%; Score 1036.5; DB 2; Length 211;	
Best Local Similarity	99.5%; Pred. No. 4.3e-94;	
Matches 186; Conservative	0; Mismatches 0; Indels 1; Gaps 1;	
QY	25 QLPPGKPEIFKCRSPNKETFTCWRRPTDGGGLPTNYSLTYHREGETLMHECPDYITGGPN 84	
DB	1 QLPPGKPEIFKCRSPNKETFTCWRRPTDGGGLPTNYSLTYHREGETLMHECPDYITGGPN 60	
QY	85 SCHFGKQYTSMTWTYIMVNAT-QMGSSFSDELYVDVTYIVQDDPPELAVKQPEDRK 143	
DB	61 SCHFGKQYTSMTWTYIMVNATQMGSSFSDELYVDVTYIVQDDPPELAVKQPEDRK 120	
QY	144 PYLWIKWSPPTLIDLKTGHTLLYEIRLKPKEAEWEIHFAQQTEFKILSLHPGQKYL 203	
DB	121 PYLWIKWSPPTLIDLKTGHTLLYEIRLKPKEAEWEIHFAQQTEFKILSLHPGQKYL 180	
QY	204 QVRCKPD 210	
DB	181 QVRCKPD 187	
RESULT 11		
ADE28697	ID ADE28697 standard; protein; 597 AA.	
XX	AC ADE28697;	
XX	29-JAN-2004 (first entry)	
DE	Human NOV18a protein - SEQ ID 74.	
XX	NOVX; antidiabetic; anorectic; cardiatic; hypotensive;	
KW	antiarteriosclerotic; virucide; antibacterial; fungicide; protozoacide;	
KW	nootropic; neuroprotective; antiparkinsonian; anticonvulsant;	
KW	osteopathic; antiarthritic; antiinflammatory; dermatological;	
KW	antiasthmatic; antilipemic; metabolic; diabetes; obesity; infectious;	
KW	anorexia; cancer; cardiovascular; hypertension; atherosclerosis;	
KW	neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune;	
KW	osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia;	
KW	neurogenesis; cell differentiation; proliferation; haemopoiesis;	
KW	wound healing; angiogenesis; gene therapy; chromosome mapping;	
KW	tissue typing; human; NOV.	
XX	Homo sapiens.	
XX	WO2003040330-A2.	
XX	15-MAY-2003.	
XX	05-NOV-2002; 2002WO-US035536.	
XX	05-NOV-2001; 2001US-0338626P.	
PR	05-DEC-2001; 2001US-0336600P.	
PR	07-DEC-2001; 2001US-0338285P.	
PR	12-DEC-2001; 2001US-0341346P.	
PR	17-DEC-2001; 2001US-0341477P.	
PR	17-DEC-2001; 2001US-0341540P.	
PR	20-DEC-2001; 2001US-0342592P.	
PR	27-DEC-2001; 2001US-0344297P.	
PR	31-DEC-2001; 2001US-0344903P.	
PR	17-APR-2002; 2002US-0373288P.	
PR	15-MAY-2002; 2002US-0380981P.	
PR	17-MAY-2002; 2002US-0381495P.	
PR	28-MAY-2002; 2002US-0383534P.	
PR	28-MAY-2002; 2002US-0383744P.	
PR	29-MAY-2002; 2002US-0383829P.	
PR	29-MAY-2002; 2002US-0384024P.	
PR	07-AUG-2002; 2002US-0401788P.	
PR	26-AUG-2002; 2002US-0406353P.	
PR	31-OCT-2002; 2002US-00287971.	
XX		
PA	(CURA-) CURAGEN CORP.	
XX	Alsbrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL;	
PI	Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;	
PI	Ellerman K, Etenberg S, Gangoli EA, Gerlach VL, Gorman L;	
PI	Grosse WM, Guo X, Hackett C, Ji W, Kekuda R, Khrantsov NV;	
PI	Lepley DM, Li L, MacDougall JR, Malyankar UM, Mazur A, Mequenev K;	
PI	Mezes PS, Miller CE, Millet I, Mishra VS, Padigara M, Paturajan M;	
PI	Pena CBA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;	
PI	Smithson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twonlow N;	
PI	Vernet CAM, Zerhusen BD, Zhong M;	
XX	WPI; 2003-441555/41.	
DR	N-PSDB; ADE28696.	
XX	New isolated NOVX polypeptides and polynucleotides, useful for	
PT	preventing, diagnosing or treating NOVX-associated disorders, e.g.	
PT	osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,	
PT	asthma, or infections.	
XX	Claim 1; SEQ ID NO 74; 447pp; English.	
XX	The invention relates to a novel isolated NOVX polypeptide. The	
CC	polypeptide of the invention demonstrates, antidiabetic, anorectic,	
CC	cardiac, hypotensive, antiarteriosclerotic, virucide, antibacterial,	
CC	fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian,	
CC	anticonvulsant, osteopathic, antiarthritic, antiinflammatory,	
CC	dermatological, antiasthmatic and antilipemic activities. The	
CC	polypeptides, nucleic acid molecules and antibodies may be useful for	
CC	treating or diagnosing diseases including metabolic disorders such as	
CC	diabetes and obesity, infectious diseases, anorexia, cancer,	
CC	cardiovascular diseases including hypertension and atherosclerosis,	
CC	neurodegenerative disorders such as Alzheimer's disease, Parkinson's	
CC	disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic	
CC	disorders, inflammatory skin disorders, asthma and dyslipidaemia.	
CC	Furthermore, the nucleic acids and polypeptides may also be used to	
CC	identify molecules that modulate or inhibit neurogenesis, cell	
CC	differentiation and proliferation, haemopoiesis, wound healing and	
CC	angiogenesis, as well as in gene therapy. Finally, the nucleic acids may	
CC	be used as hybridisation probes, in chromosome mapping, tissue typing,	
CC	preventive medicine and pharmacogenomics. The current sequence is that of	
CC	the human NOV protein of the invention.	
XX	Sequence 597 AA;	
SQ	Query Match 84.6%; Score 987; DB 7; Length 597;	
	Best Local Similarity 87.7%; Pred No. 1.2e-88;	
	Matches 185; Conservative 0; Mismatches 0; Indels 26; Gaps 2;	
QY	1 MXENVASATVFTLLFLNTCLNGQLPFGKPEIFKCRSPNKETFTCWRRPTDGGGLP 60	
DB	1 MXENVASATVFTLLFLNTCLNGQLPFGKPEIFKCRSPNKETFTCWRRPTDGGGLP 58	
QY	61 SLTYHREGETLMHECPDYITGPNNSCHFGKQYTSMTWTYIMVNAT-QWSSFSDELYVD 119	
DB	59 -----NSCHFGKQYTSMTWTYIMVNATNQWSSFSDELYVD 95	
QY	120 VTYIVQPPPLELAVKQPEDRKPYLWKSPPTLIDLKTGHTLLYEIRLKPKEAEW 179	
DB	96 VTYIVQPPPLELAVKQPEDRKPYLWKSPPTLIDLKTGHTLLYEIRLKPKEAEW 155	
QY	180 EIHFAQQTEFKILSLHPGQKYLQVRCKPD 210	
DB	156 EIHFAQQTEFKILSLHPGQKYLQVRCKPD 186	
RESULT 12		
AA96918	ID AA96918 standard; protein; 134 AA.	
XX	AC AA96918;	
XX	31-OCT-2000 (first entry)	

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XX DE Soluble human prolactin receptor clone E.
XX KW hPRLR; soluble; prolactin receptor; gastrointestinal; splice variant;
XX KW binding protein; prolactin; growth hormone; agonist; antagonist.
XX OS Homo sapiens.
XX PN US6083714-A.
XX PD 04-JUL-2000.
XX PF 26-FEB-1997; 97US-00806597.
XX PR 29-FEB-1996; 96US-0012503P.
XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX PI Kelly PA, Nagano M;
XX PI WPI; 2000-464339/40.
XX DR N-PSDB; AAA53590.
XX DR
XX PT New soluble prolactin receptors useful as human growth hormone binding
XX PT protein and in x-ray crystallographic analysis for developing molecular
XX PT models which define the tertiary structure of the hormone-binding
XX PT domains.
XX PS Claim 1; Col 31-32; 26pp; English.
XX PS
XX CC Soluble human prolactin receptor (hPRLR) isoforms have been isolated from
XX CC the human gastrointestinal tract. The isoforms have a deletion in the
XX CC extra- or intracellular domain and are thought to be generated by
XX CC alternative splicing, since four clones (A, B, C and E) precisely lack
XX CC one or two exons. Except for clone C, the deletion in all other clones
XX CC resulted in a frameshift and produced a stop codon before the
XX CC transmembrane domain. The soluble hPRLR may be used as a binding protein
XX CC for human prolactin and/or human growth hormone, which can be used in
XX CC diagnostics for the detection and measurement of the binding ligand or in
XX CC therapeutics for binding to human prolactin and/or human growth hormone
XX CC to retard or inhibit their hormone activities. They may also be used in
XX CC place of monoclonal antibodies to provide solution-based radioligand
XX CC receptor assays, in receptor sandwich or enzymatic assays, and in x-ray
XX CC crystallographic analysis to develop molecular models, which define the
XX CC tertiary structure of the hormone-binding domains, where such information
XX CC would provide insight into the structure of the actual contact between a
XX CC hormone and its receptor. This structural information would be useful in
XX CC the design of peptides which have prolactin or growth hormone-like
XX CC agonistic or antagonistic activity
XX SQ Sequence 134 AA;

Query Match 58.2%; Score 679; DB 3; Length 134;
Best Local Similarity 96.9%; Pred. No. 5.1e-59;
Matches 125; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

QY 1 MKENVASATVFTLLFLNLTCLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60
DB 1 MKENVASATVFTLLFLNLTCLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60
QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAAT-QMGSSFSDELVD 119
DB 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAATQMGSSFSDELVD 120
QY 120 VTYIVQDP 128
DB 121 VTYI---DP 126

RESULT 13
AAAY95526
ID AAAY95526 standard; protein; 134 AA.

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XX AC AAAY95526;
XX DT 10-OCT-2000 (first entry)
XX DE Soluble isoform of human prolactin receptor.
XX KW Prolactin receptor; PRLR; human; isoform.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..24
XX FT Protein /label= Signal_peptide
XX FT 25..134 /label= Soluble_PRLR
XX PN US6083753-A.
XX PD 04-JUL-2000.
XX PF 14-NOV-1997; 97US-00970428.
XX PR 29-FEB-1996; 96US-0012503P.
XX PR 26-FEB-1997; 97US-00806597.
XX PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX PI Kelly PA, Nagano M;
XX PI WPI; 2000-464346/40.
XX DR N-PSDB; AAA49979.
XX PT New recombinant DNA having a segment encoding a signal peptide joined
XX PT translationally to a segment encoding a soluble human prolactin receptor
XX PT useful as a hormone growth hormone binding protein, and in x-ray
XX PT crystallographic analysis.
XX PS Claim 1; Col 32-33; 27pp; English.
XX CC The present sequence is that of a newly identified soluble isoform of the
XX CC human prolactin receptor (PRLR). DNA encoding this isoform (see AAA49979)
XX CC lacks exon 6 of the full-length receptor, resulting in a frameshift that
XX CC produces a stop codon before the transmembrane domain. The putative
XX CC secreted protein product has a lower affinity for prolactin than the wild
XX CC -type receptor due to the lack of a WS motif, but it retains 5 cysteine
XX CC residues that are crucial for ligand binding. 6 Isoforms (see AAA49976-
XX CC 82) of human PRLR have been identified in human colonic Caco-2 and human
XX CC breast cancer T-47D cells. Recombinant DNA molecules encoding the soluble
XX CC PRLR proteins are provided, as well as expression vectors and host cells.
XX CC The soluble PRLRs may be used as binding proteins for human prolactin
XX CC and/or human growth hormone, which can be useful in diagnostics for the
XX CC detection and measurement of the binding ligand, or in therapeutics for
XX CC binding to human prolactin and/or human growth hormone to retard or
XX CC inhibit their hormone activities. They may also be used in place of
XX CC monoclonal antibodies to provide solution-based radioligand receptor
XX CC assays, in receptor sandwich or enzymatic assays, and in x-ray
XX CC crystallographic analysis to develop molecular models that define the
XX CC tertiary structure of the hormone-binding domains, where such information
XX CC would provide insight into the structure of the actual contact between a
XX CC hormone and its receptor. This structural information would be useful in
XX CC the design of peptides that have prolactin or growth hormone-like
XX CC agonistic or antagonistic activity
XX SQ Sequence 134 AA;

Query Match 58.2%; Score 679; DB 3; Length 134;
Best Local Similarity 96.9%; Pred. No. 5.1e-59;
Matches 125; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

QY 1 MKENVASATVFTLLFLNLTCLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60

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Db      1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTTCWWRPGTDGGLPTNY 60
Qy      61 SLTYHREGELTHMECPDYITGGNSCHFGKQYTSMTWRTYIMVNAT-QMGSSFSDELYVD 119
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Qy      120 VTYIVQDPD 128
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Db      121 VTYI---DP 126

RESULT 14
AAR93121
ID AAR93121 standard; protein; 606 AA.
XX AC AAR93121;
XX DT 10-OCT-1996 (first entry)
XX DE Tilapia prolactin receptor (mature form).
XX KW Fish prolactin; tiPRL; receptor; hormone; agonist; antagonist;
KW reproductive cycle synchronisation; teleost; bony fish; Cypriniformes.
XX OS Oreochromis niloticus.
XX FH Key Location/Qualifiers
FH Protein 1..606
FH Domain 1..210
FH /label= prolactin_receptor
FH /label= extracellular
FH /note= "comprises 5 Cys residues"
FH Modified-site 68..70
FH /label= glycosylation_site
FH /note= "potential"
FH Modified-site 77..79
FH /label= glycosylation_site
FH /note= "potential"
FH Binding-site 192..196
FH /label= ligand_binding_motif
FH /note= "conforms to Trp-Ser-Xaa-Trp-Ser consensus"
FH Domain 211..234
FH /label= transmembrane
FH Domain 235..606
FH /label= cytoplasmic
FH /note= "slightly longer than mammalian PRL receptor
FH cytoplasmic domain"
FH Region 245..250
FH /label= Box_1
FH /note= "proline-rich region highly conserved among
FH receptors for cytokines, growth hormones and prolactin
FH and is critical for signal transduction"
XX FN FR2724181-A1.
XX PD 08-MAR-1996.
XX PF 01-SEP-1994; 94FR-00010535.
XX PR 01-SEP-1994; 94FR-00010535.
XX PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX PI Kelly PA, Edery M, Prunet P, Sandra O;
XX WPI: 1996-153124/16.
XX N-PSDB; AAT17141.
XX Fish prolactin receptor - useful for detecting prolactin agonists and
XX antagonists.
XX Claim 5; Page 20-21; 35pp; French.

```

```

CC A cDNA sequence coding for a fish prolactin (PRL) receptor was isolated
CC from a Oreochromis niloticus (tilapia) kidney cDNA expression library
CC following screening with radioactive tiPRL. The cDNA insert was found to
CC contain an open reading frame for a 630 amino acid protein. The mature
CC protein (606 amino acids) has estimated mol. wt. 68.2 kDa and isoelectric
CC point 5.53. Transformed eukaryotic cells expressing the PRL receptor are
CC useful for identifying agonists and antagonists of PRL which have
CC potential applications in fish farming, e.g. for synchronising
CC reproductive cycles. The present sequence is that of the mature PRL
CC receptor from tilapia
XX SQ Sequence 606 AA;

Query Match 47.1%; Score 549.5; DB.2; Length 606;
Best Local Similarity 54.6%; Pred. No. 2.2e-45;
Matches 101; Conservative 26; Mismatches 55; Indels 3; Gaps 3;

Qy      28 PGKPEIFKCRSPNKETFTTCWWRPGTDGGLPTNYSLTYHREGELTHMECPDYITGGNSCH 87
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Db      5 PGKPEIFKCRSPNKETFTTCWWRPGTDGGLPTNYALYKRGSDVVEHPCDVTAGKNSCF 64
Qy      88 PGKQVTSWRYIIMVNATQ-MGSSFSDELYVDYIVQDPDPLEAVEVKQPEDRKPYL 146
        |||||
Db      65 FNKNNTLIWSYNTTVAATNALGKTYSDQIDIVVYIVQHPPEKLEVTVMK-DQGWPF 123
Qy      147 WIKNSPPTLIDLKTGWFTLLYEIRLKPE-KAAAEIHFAGQOTEFKILSLHPGQKYLQV 205
        |||||
Db      124 RVSWEPKADTRSGWITLIYELRVKLEDESEWENHAAGQKMFISLSGGTYLIQV 183
Qy      206 RCKPD 210
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Db      184 RCKPD 188

RESULT 15
AAR93120
ID AAR93120 standard; protein; 630 AA.
XX AC AAR93120;
XX DT 09-OCT-1996 (first entry)
XX DE Tilapia prolactin receptor precursor.
XX KW Fish prolactin; tiPRL; receptor; hormone; agonist; antagonist;
KW reproductive cycle synchronisation; teleost; bony fish; Cypriniformes.
XX OS Oreochromis niloticus.
XX FH Key Location/Qualifiers
FH Protein 25..630
FH Domain 25..234
FH /label= prolactin_receptor
FH /label= extracellular
FH /note= "comprises 5 Cys residues"
FH Modified-site 92..94
FH /label= glycosylation_site
FH /note= "potential"
FH Modified-site 101..103
FH /label= glycosylation_site
FH /note= "potential"
FH Binding-site 216..220
FH /label= ligand_binding_motif
FH /note= "conforms to Trp-Ser-Xaa-Trp-Ser consensus"
FH Domain 235..258
FH /label= transmembrane
FH Domain 259..630
FH /label= cytoplasmic
FH /note= "slightly longer than mammalian PRL receptor
FH cytoplasmic domain"
FH Region 269..274
FH /label= Box_1
FH /note= "proline-rich region highly conserved among

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receptors for cytokines, growth hormones and prolactin  
and is critical for signal transduction"

FR2724181-A1.

08-MAR-1996.

01-SEP-1994; 94FR-00010535.

01-SEP-1994; 94FR-00010535.

(INRM ) INSERM INST NAT SANTE &amp; RECH MEDICALE.

Kelly PA, Edery M, Prunet P, Sandra O;

WPI; 1996-153124/16.

N-PSDB; AAT17141.

Fish prolactin receptor - useful for detecting prolactin agonists and  
antagonists.

Example; Page 15-16; 35pp; French.

A cDNA sequence coding for a fish prolactin (PRL) receptor was isolated  
from a Oreochromis niloticus (tilapia) kidney cDNA expression library  
following screening with radioactive tPRL. The cDNA insert was found to  
contain an open reading frame for a 630 amino acid protein. The mature  
protein (606 amino acids) has estimated mol. wt. 68.2 kDa and isoelectric  
point 5.53. Transformed eukaryotic cells expressing the PRL receptor are  
useful for identifying agonists and antagonists of PRL which have  
potential applications in fish farming, e.g. for synchronising  
reproductive cycles. The present sequence is that of the precursor for  
the PRL receptor from tilapia

SQ Sequence 630 AA;

Query Match

47.1%; Score 549.5; DB 2; Length 630;

Best Local Similarity 54.6%; Pred. No. 2.3e-45;

Matches 101; Conservative 26; Mismatches 55; Indels 3; Gaps 3;

QY 28 PGKPEIFKCRSPNKETFTCWRRGTDGGLPTNYSLTYHREGTLMHECPDYITGGPNSCH 87

Db 29 PGKPTIKCRSPKEFTFTCWKFGSDGGLPTTYALYRKESDGVHECPDHTAGKNSCF 88

QY 88 FGQYTSMTMRTYIMVNATO-MGSPFSDLYVDVTYIVQDPPELAVEVKQPEDRKPYL 146

Db 89 FNKNNTLIWVSNITVYATNALGKTYSDPDIDVYVIVQHPPEKLEVTVMK-DQGWPF 147

QY 147 WIKWSPTLIDKGTGFTLLYIRLKPE-KAAEWEIHFAGQQTETKILSLHPGQKYLIVQV 205

Db 148 RVSWEPKPRADIRSGWITLIYELRVKLEDESEWENHAGQOQMFNIFSLRSGGTYLIQV 207

QY 206 RCKPD 210

Db 208 RCKPD 212

Search completed: May 12, 2004, 16:17:27  
Job time : 62 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 12, 2004, 16:19:02 ; Search time 45 Seconds  
(without alignments)  
1295,312 Million cell updates/sec

Title: US-10-029-079-3  
Perfect score: 1166  
Sequence: 1 MKENVASATVFTLLFLNTCL.....KILSLHPGQKYLQVVRCKPD 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	1166	100.0	210	13	US-10-029-079-3	Sequence 3, Appl1
2	1155.5	99.1	622	12	US-10-058-270A-40	Sequence 40, Appl
3	1155.5	99.1	622	14	US-10-177-293-373	Sequence 373, App
4	1155.5	99.1	622	15	US-10-295-027-112	Sequence 112, App
5	1155.5	99.1	622	15	US-10-295-027-744	Sequence 744, App
6	987	84.6	597	12	US-10-287-971-74	Sequence 74, Appl
7	297	25.5	389	9	US-09-880-578-25	Sequence 25, Appl
8	297	25.5	389	9	US-09-880-578-26	Sequence 26, Appl
9	296	25.4	303	9	US-09-880-578-21	Sequence 21, Appl
10	296	25.4	385	9	US-09-880-578-20	Sequence 20, Appl
11	296	25.4	388	9	US-09-880-578-17	Sequence 17, Appl
12	296	25.4	389	9	US-09-880-578-27	Sequence 27, Appl
13	296	25.4	389	9	US-09-880-578-31	Sequence 31, Appl
14	296	25.4	422	9	US-09-880-578-2	Sequence 2, Appl1
15	295	25.3	389	9	US-09-880-578-30	Sequence 30, Appl

294 25.2 389 9 US-09-880-578-24 Sequence 24, Appl1

294 25.2 389 9 US-09-880-578-28 Sequence 28, Appl1

294 25.2 389 9 US-09-880-578-29 Sequence 29, Appl1

293 25.1 303 9 US-09-880-578-23 Sequence 23, Appl1

293 25.1 350 9 US-09-037-657-25 Sequence 25, Appl1

293 25.1 389 9 US-09-880-578-22 Sequence 22, Appl1

293 25.1 392 9 US-09-880-578-18 Sequence 18, Appl1

293 25.1 404 14 US-10-252-958-2 Sequence 2, Appl1

293 25.1 410 14 US-10-247-463-4 Sequence 4, Appl1

293 25.1 421 9 US-09-037-657-44 Sequence 44, Appl1

293 25.1 422 9 US-09-866-028-32 Sequence 32, Appl1

293 25.1 422 9 US-09-944-449-32 Sequence 32, Appl1

293 25.1 422 9 US-09-944-457-32 Sequence 32, Appl1

293 25.1 422 9 US-09-944-862-32 Sequence 32, Appl1

293 25.1 422 9 US-09-945-587-32 Sequence 32, Appl1

293 25.1 422 9 US-09-945-015-32 Sequence 32, Appl1

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293 25.1 422 9 US-09-943-762-32 Sequence 32, Appl1

293 25.1 422 9 US-09-943-654-32 Sequence 32, Appl1

293 25.1 422 9 US-09-943-851A-32 Sequence 32, Appl1

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293 25.1 422 9 US-09-944-896-32 Sequence 32, Appl1

293 25.1 422 9 US-09-944-944-32 Sequence 32, Appl1

293 25.1 422 9 US-09-944-929-32 Sequence 32, Appl1

293 25.1 422 9 US-09-944-907-32 Sequence 32, Appl1

293 25.1 422 10 US-09-944-864-32 Sequence 32, Appl1

293 25.1 422 10 US-09-944-852-32 Sequence 32, Appl1

## ALIGNMENTS

RESULT 1

US-10-029-079-3

Sequence 3, Application US/10029079

Publication No. US20020119154A1

GENERAL INFORMATION:

APPLICANT: Clevenger, Charles V

APPLICANT: Kline, J. Bradford

TITLE OF INVENTION: Composition and Method for Modulating Somatolactogenic Function

FILE REFERENCE: PENN-0795

CURRENT APPLICATION NUMBER: US/10/029,079

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 60/258,285

PRIOR FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 210

TYPE: PRT

ORGANISM: Homo sapien

US-10-029-079-3

Query Match 100.0%; Score 1166; DB 13; Length 210;

Best Local Similarity 100.0%; Pred. No. 1.9e-106;

Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKENVASATVFTLLFLNTCLNGOLPPGKPEIFKCRSPNKETFTCMWRPGTDGGLPTNY 60

Db 1 MKENVASATVFTLLFLNTCLNGOLPPGKPEIFKCRSPNKETFTCMWRPGTDGGLPTNY 60

QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWMRTYIMMVNATQWGSFSDLYVDV 120

Db 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWMRTYIMMVNATQWGSFSDLYVDV 120

QY 121 TVIVOPDPLELAVKQPEKPYLWIKWSPPTLIDIKTGWFTLLYIRLKPXAAWE 180

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RESULT 2

US-10-058-270A-40  
 ; Sequence 40, Application US/10058270A  
 ; Publication No. US20040029114A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mack, David H.  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Afar, Daniel  
 ; APPLICANT: Eos Biotechnology, Inc.  
 ; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and  
 ; FILE REFERENCE: 018501-005210US  
 ; CURRENT APPLICATION NUMBER: US/10/058,270A  
 ; CURRENT FILING DATE: 2002-01-24  
 ; PRIOR APPLICATION NUMBER: US 60/263,965  
 ; PRIOR FILING DATE: 2001-01-24  
 ; PRIOR APPLICATION NUMBER: US 60/265,928  
 ; PRIOR FILING DATE: 2001-02-02  
 ; PRIOR APPLICATION NUMBER: US 09/829,472  
 ; PRIOR FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/282,698  
 ; PRIOR FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/288,590  
 ; PRIOR FILING DATE: 2001-05-04  
 ; PRIOR APPLICATION NUMBER: US 60/294,443  
 ; PRIOR FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 141  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 40  
 ; LENGTH: 622  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-058-270A-40

Query Match 99.1%; Score 1155.5; DB 12; Length 622;  
 Best Local Similarity 99.5%; Pred. No. 7.7e-105;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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 Db 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60  
 QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMVNAT-QMGSSFSDELVD 119  
 Db 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMVNATQMGSSFSDELVD 120  
 QY 120 VTIYVQDPPLELAVEKQEDRKPYLWIKWSPPTLIDKTGFTLLYRILKPEKAAEW 179  
 Db 121 VTIYVQDPPLELAVEKQEDRKPYLWIKWSPPTLIDKTGFTLLYRILKPEKAAEW 180  
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RESULT 3

US-10-177-293-373  
 ; Sequence 373, Application US/10177293  
 ; Publication No. US20030124128A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lillie, James  
 ; APPLICANT: Zhao, Xumei  
 ; APPLICANT: Gannavarpu, Manjula  
 ; APPLICANT: Kamatkar, Shubhangi  
 ; APPLICANT: Mertens, Maureen  
 ; APPLICANT: Myer, Vic  
 ; APPLICANT: Wang, Youzhen  
 ; APPLICANT: Xu, Yongyao

; APPLICANT: Hoersch, Sebastian  
 ; APPLICANT: Monahan, John  
 ; APPLICANT: Meyers, Rachel E.  
 ; APPLICANT: Bast Jr., Robert C.  
 ; APPLICANT: Hortobagyi, Gabriel N.  
 ; APPLICANT: Fuzstai, Lajos  
 ; APPLICANT: Meric, Funda  
 ; APPLICANT: Sahin, Aysegul  
 ; APPLICANT: Mills, Gordon B.  
 ; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,  
 ; FILE REFERENCE: MRI-038  
 ; CURRENT APPLICATION NUMBER: US/10/177,293  
 ; CURRENT FILING DATE: 2002-06-21  
 ; PRIOR APPLICATION NUMBER: US 60/299,887  
 ; PRIOR FILING DATE: 2001-06-21  
 ; PRIOR APPLICATION NUMBER: US 60/301,572  
 ; PRIOR FILING DATE: 2001-06-27  
 ; PRIOR APPLICATION NUMBER: US 60/306,501  
 ; PRIOR FILING DATE: 2001-07-18  
 ; PRIOR APPLICATION NUMBER: US 60/325,002  
 ; PRIOR FILING DATE: 2001-09-25  
 ; PRIOR APPLICATION NUMBER: US 60/362,585  
 ; PRIOR FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: US 60/xxx,xxx  
 ; PRIOR FILING DATE: 2002-05-14  
 ; NUMBER OF SEQ ID NOS: 506  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 373  
 ; LENGTH: 622  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-177-293-373

Query Match 99.1%; Score 1155.5; DB 14; Length 622;  
 Best Local Similarity 99.5%; Pred. No. 7.7e-105;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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 Db 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60  
 QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMVNAT-QMGSSFSDELVD 119  
 Db 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMMRTYIMMVNATQMGSSFSDELVD 120  
 QY 120 VTIYVQDPPLELAVEKQEDRKPYLWIKWSPPTLIDKTGFTLLYRILKPEKAAEW 179  
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 Db 181 EIHFGAGQOTEFKILSLHPGQKYLQVRCRCPD 211

RESULT 4

US-10-295-027-112  
 ; Sequence 112, Application US/10295027  
 ; Publication No. US20030232350A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Afar, Daniel  
 ; APPLICANT: Aziz, Natasha  
 ; APPLICANT: Ginsberg, Wendy M.  
 ; APPLICANT: Gish, Kurt C.  
 ; APPLICANT: Glynn, Richard  
 ; APPLICANT: Hevezi, Peter A.  
 ; APPLICANT: Mack, David H.  
 ; APPLICANT: Murray, Richard  
 ; APPLICANT: Watson, Susan R.  
 ; APPLICANT: Eos Biotechnology, Inc.  
 ; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
 ; FILE REFERENCE: 018501-012500US



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; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 622
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-10-295-027-112

Query Match          99.1%; Score 1155.5; DB 15; Length 622;
Best Local Similarity 99.5%; Pred. No. 7.7e-105;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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D5 61 SLVYHREGETLMHECPDYITGGNSCHFGKQYTSWRTYIMVNATQMGSSFSDELYVD 120
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D5 181 EHFAGQOTEFKILSLHPGQKYLQVRCRKP 211

RESULT 5
US-10-295-027-744
; Sequence 744, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
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; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 744
; LENGTH: 622
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-10-295-027-744

Query Match          99.1%; Score 1155.5; DB 15; Length 622;
Best Local Similarity 99.5%; Pred. No. 7.7e-105;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
D5 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
QY 61 SLVYHREGETLMHECPDYITGGNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVD 119
D5 61 SLVYHREGETLMHECPDYITGGNSCHFGKQYTSWRTYIMVNATQMGSSFSDELYVD 120
QY 120 VTYIVQDPPELEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYELRLKPEKAAEW 179
D5 121 VTYIVQDPPELEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYELRLKPEKAAEW 180
QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRKP 210
D5 181 EHFAGQOTEFKILSLHPGQKYLQVRCRKP 211

RESULT 6
US-10-287-971-74
; Sequence 74, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-480A
; CURRENT APPLICATION NUMBER: US/10/287,971
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
```

; PRIOR APPLICATION NUMBER: 60/406,181  
; PRIOR FILING DATE: 2002-08-26  
; NUMBER OF SEQ ID NOS: 397  
; SOFTWARE: Curaseq1ist version 0.1  
; SEQ ID NO 74  
; LENGTH: 597  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-971-74

Query Match 84.68; Score 987; DB 12; Length 597;  
Best Local Similarity 87.74; Pred. No. 2.7e-88;  
Matches 185; Conservative 0; Mismatches 26; Gaps 2;  
QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTTCWRPFGTDGGLPTNY 60  
DB 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTTCWRPFGTDGGLPT-- 58  
QY 61 SLTYHREGETLMHECPDYITGGNSCHFGKQYTSMTWRTYIMMVNAT-QVGSFSDLYVD 119  
DB 59 -----NSCHFGKQYTSMTWRTYIMMVNATNQGSFSDLYVD 95  
QY 120 VTIIVQDPPLLEAVEVKQPEDRKPYLWIKWSPTLIDLTGTFLLYIRLKPKEAAEW 179  
DB 96 VTIIVQDPPLLEAVEVKQPEDRKPYLWIKWSPTLIDLTGTFLLYIRLKPKEAAEW 155  
QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRKP 210  
DB 156 EHFAGQOTEFKILSLHPGQKYLQVRCRKP 186

## RESULT 7

US-09-880-578-25  
; Sequence 25, Application US/09880578  
; Patent No. US20020045733A1  
; GENERAL INFORMATION:

APPLICANT: Lok, Si

Presnell, Scott R.  
Jelmsberg, Anna C.  
Gilbert, Teresa  
Foster, Donald C.  
Adams, Robyn L.  
Lehner, Joyce M.

TITLE OF INVENTION: MAMMALIAN ZCYTORS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics  
STREET: 1201 Eastlake Ave East  
CITY: Seattle  
STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/880,578

FILING DATE: 13-Jun-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: &lt;Unknown&gt;

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX: &lt;Unknown&gt;

INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 389 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-880-578-25

Query Match 25.58; Score 297; DB 9; Length 389;  
Best Local Similarity 38.08; Pred. No. 1.1e-20;  
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;  
QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTTCWRPFGTDGG--LPTNYSILTYHREGETLM 72  
DB 86 ILAGSCLYVG-LPEKFPWISCHSKNMKDLTCRWTPGAHGETFLHTNYSILKYKLWVGQD 144  
QY 73 HECDPYITGGNSCHFGKQYTSMTWRTYIMMVNAT-QVGSFSDLYVDVTVIIVQDPPLF 131  
DB 145 NTCEDYHTVGFHSCHPKD-LALFTPYEIWVEATNRLGSARSDVLTLDILDVVTDDPPD 203  
QY 132 LAV-EVQKQPEDRKPYLWIKWSPTLIDLTGTFLLYIRLKPKEAAEW-IHFAGQOTE 189  
DB 204 VHSRVGLEDQLSVRV--SPALKDF---LFQAKYQIRYRVEDSDVWKVVDVDSNQT 258  
QY 190 FKILSLHPGQKYLQVRCRKP 209  
DB 259 CRLAGLKPQTVYFVQVRCNP 278

## RESULT 8

US-09-880-578-26  
; Sequence 26, Application US/09880578  
; Patent No. US20020045733A1  
; GENERAL INFORMATION:

APPLICANT: Lok, Si

Presnell, Scott R.  
Jelmsberg, Anna C.  
Gilbert, Teresa  
Foster, Donald C.  
Adams, Robyn L.  
Lehner, Joyce M.

TITLE OF INVENTION: MAMMALIAN ZCYTORS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zymogenetics  
STREET: 1201 Eastlake Ave East  
CITY: Seattle  
STATE: WA

COUNTRY: USA

ZIP: 98102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/880,578

FILING DATE: 13-Jun-2001

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: &lt;Unknown&gt;

FILING DATE: &lt;Unknown&gt;

ATTORNEY/AGENT INFORMATION:

NAME: Lunn, Paul G

REGISTRATION NUMBER: 32,743

REFERENCE/DOCKET NUMBER: 96-22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-442-6627

TELEFAX: 206-442-6678

TELEX: &lt;Unknown&gt;

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

```
;
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-880-578-26

Query Match      25.5%; Score 297; DB 9; Length 389;
Best Local Similarity 38.0%; Pred. No. 1.1e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFLNTCLLNGQLPCKPEIFKCRSPNKETFTCWRRPGTDG--LPTNYSLTTHREGETLM 72
DB 86 ILAGSCLVYG-LPPEKPVNISCSKMKDLTCRWTPCAHGETFLHTNYSLKYLKRWYQD 144
QY 73 HECPDYITGGPNSCHFGKQVTSWRTYIMVNAT-QMGSSFSDELVDVTVIVQDPDPLE 131
DB 145 NTCEYHTVGHPSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDILDVTTDPPD 203
QY 132 LAV-EVKQPEDRKPYLWIKMSPTLIDLKTGWFLLYIIRLKPEKAAWE-IHFAGQOTE 189
DB 204 VHSVSRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVSDVDWKVDDVSNQTS 258
QY 190 FKILSLHFGOKYLVQVRCKP 209
DB 259 CRLAGLKPGTYFVQVRCP 278

RESULT 9
US-09-880-578-21
; Sequence 21, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelmeberg, Anna C.
; Gilbert, Teresa
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-880-578-21

Query Match      25.4%; Score 296; DB 9; Length 303;
Best Local Similarity 38.0%; Pred. No. 1.1e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFLNTCLLNGQLPCKPEIFKCRSPNKETFTCWRRPGTDG--LPTNYSLTTHREGETLM 72
DB 86 ILAGSCLVYG-LPPEKPVNISCSKMKDLTCRWTPCAHGETFLHTNYSLKYLKRWYQD 144
QY 73 HECPDYITGGPNSCHFGKQVTSWRTYIMVNAT-QMGSSFSDELVDVTVIVQDPDPLE 131
DB 145 NTCEYHTVGHPSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDILDVTTDPPD 203
QY 132 LAV-EVKQPEDRKPYLWIKMSPTLIDLKTGWFLLYIIRLKPEKAAWE-IHFAGQOTE 189
DB 204 VHSVSRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVSDVDWKVDDVSNQTS 258
QY 190 FKILSLHFGOKYLVQVRCKP 209
DB 259 CRLAGLKPGTYFVQVRCP 278

RESULT 10
US-09-880-578-20
; Sequence 20, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelmeberg, Anna C.
; Gilbert, Teresa
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-880-578-20

Query Match      25.4%; Score 296; DB 9; Length 385;
Best Local Similarity 38.0%; Pred. No. 1.4e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPNTNYSITYHREGETLM 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 86 ILAGSCLVVG-LPPEKPVNISCWSKNMKDLTCRTWTPGAHGETLHTNYSILKYKLRWYGQD 144
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 HECPDYITGPNCHFGKQYTSWRTYIMVNAT-QMGSSFSDELVDVTVYIVQDPDPPL 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 145 NTCBEYHTVGPCHPKD-LALFTPYEIWVEATNLGARSADVLTDLILDVVTTPDPP 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 LAV-EVKQPEDRKPYLWKMSPTLIDLKTGWFTLLYEIRLKEKAAEWE-IHFAGQOTE 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 204 VHSRVGGLDQLSVRWV--SPALKDF---LFQAKYQIRYRVEDSDVWKVDDVSNQTS 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 FKILSLHPGQKYLQVRCKP 209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 259 CRLAGLKPGTVYFVQRCNP 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-09-880-578-17
; Sequence 17, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelneberg, Anna C.
; Gilbert, Teresa
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 388 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-880-578-17

Query Match      25.4%; Score 296; DB 9; Length 388;
Best Local Similarity 38.0%; Pred. No. 1.4e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPNTNYSITYHREGETLM 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 89 ILAGSCLVVG-LPPEKPVNISCWSKNMKDLTCRTWTPGAHGETLHTNYSILKYKLRWYGQD 147
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 HECPDYITGPNCHFGKQYTSWRTYIMVNAT-QMGSSFSDELVDVTVYIVQDPDPPL 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 148 NTCBEYHTVGPCHPKD-LALFTPYEIWVEATNLGARSADVLTDLILDVVTTPDPP 206
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 LAV-EVKQPEDRKPYLWKMSPTLIDLKTGWFTLLYEIRLKEKAAEWE-IHFAGQOTE 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 207 VHSRVGGLDQLSVRWV--SPALKDF---LFQAKYQIRYRVEDSDVWKVDDVSNQTS 261
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 FKILSLHPGQKYLQVRCKP 209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 CRLAGLKPGTVYFVQRCNP 281
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
US-09-880-578-27
; Sequence 27, Application US/09880578
; Patent No. US20020045733A1
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; Presnell, Scott R.
; Jelneberg, Anna C.
; Gilbert, Teresa
; Foster, Donald C.
; Adams, Robyn L.
; Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,578
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-09-880-578-31  
Query Match 25.4%; Score 296; DB 9; Length 389;  
Best Local Similarity 37.5%; Pred. No. 1.4e-20;  
Matches 75; Conservative 29; Mismatches 84; Indels 12; Gaps 8;  
QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTTHREGETLM 72  
DB 86 ILASGCLYVG-LPPEKPNVNSKSKMKDLTCRWTFGAHGETFLHTNYSKYLRLWYGQD 144  
QY 73 HECPDYITGPNCHFGKQYTSWMRTYIMMNAT-QMGSSFSDELYVDVTVYVQDPPLP 131  
DB 145 NTCEEYHTVGPCHPKD-LALFTPEYIWEATNRLGSSRSVDLTLDILDVTTDPPD 203  
QY 132 LAV-EVQPEDEKPYLWIKWSPPTLIDLKTGFTLLYEIRLKPKEAAEWE-IHFAGQOTE 189  
DB 204 VHSRVGGLDQLSVRWV--SPALKDF---LFOAKYQIRYRVEDSDVKVDDVSNQTS 258  
QY 190 FKILSLHPGOKYLVQVRCKP 209  
DB 259 CRLGLKPGTVYFVQVRCP 278  
RESULT 14  
US-09-880-578-2  
; Sequence 2, Application US/09880578  
; Patent No. US20020045733A1  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; Presnell, Scott R.  
; Jelmeberg, Anna C.  
; Gilbert, Teresa  
; Foster, Donald C.  
; Adams, Robyn L.  
; Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zymogenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/880,578  
; FILING DATE: 13-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 422 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal

MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-880-578-27  
Query Match 25.4%; Score 296; DB 9; Length 389;  
Best Local Similarity 38.0%; Pred. No. 1.4e-20;  
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;  
QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLTTHREGETLM 72  
DB 86 ILASGCLYVG-LPPEKPNVNSKSKMKDLTCRWTFGAHGETFLHTNYSKYLRLWYGQD 144  
QY 73 HECPDYITGPNCHFGKQYTSWMRTYIMMNAT-QMGSSFSDELYVDVTVYVQDPPLP 131  
DB 145 NTCEEYHTVGPCHPKD-LALFTPEYIWEATNRLGSSRSVDLTLDILDVTTDPPD 203  
QY 132 LAV-EVQPEDEKPYLWIKWSPPTLIDLKTGFTLLYEIRLKPKEAAEWE-IHFAGQOTE 189  
DB 204 VHSRVGGLDQLSVRWV--SPALKDF---LFOAKYQIRYRVEDSDVKVDDVSNQTS 258  
QY 190 FKILSLHPGOKYLVQVRCKP 209  
DB 259 CRLGLKPGTVYFVQVRCP 278  
RESULT 13  
US-09-880-578-31  
; Sequence 31, Application US/09880578  
; Patent No. US20020045733A1  
; GENERAL INFORMATION:  
; APPLICANT: Lok, Si  
; Presnell, Scott R.  
; Jelmeberg, Anna C.  
; Gilbert, Teresa  
; Foster, Donald C.  
; Adams, Robyn L.  
; Lehner, Joyce M.  
; TITLE OF INVENTION: MAMMALIAN ZCYTORS  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Zymogenetics  
; STREET: 1201 Eastlake Ave East  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98102  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/880,578  
; FILING DATE: 13-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lunn, Paul G  
; REGISTRATION NUMBER: 32,743  
; REFERENCE/DOCKET NUMBER: 96-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-442-6627  
; TELEFAX: 206-442-6678  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 389 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:17:31 ; Search time 183 Seconds  
(without alignments)  
1120.061 Million cell updates/sec

Title: US-10-029-079-3  
Perfect score: 1166  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Parents AA Main:\*

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- 3: /cgn2\_6/prodata/2/paa/US07 COMB.pep.\*
- 4: /cgn2\_6/prodata/2/paa/US08 COMB.pep.\*
- 5: /cgn2\_6/prodata/2/paa/US08 COMB.pep.\*
- 6: /cgn2\_6/prodata/2/paa/US08 COMB.pep.\*
- 7: /cgn2\_6/prodata/2/paa/US08 COMB.pep.\*
- 8: /cgn2\_6/prodata/2/paa/US08 COMB.pep.\*
- 9: /cgn2\_6/prodata/2/paa/US08 COMB.pep.\*
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- 30: /cgn2\_6/prodata/2/paa/US08 COMB.pep.\*
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- 32: /cgn2\_6/prodata/2/paa/US08 COMB.pep.\*
- 33: /cgn2\_6/prodata/2/paa/US08 COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
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1	1166	100.0	210	26	US-10-029-079-3	Sequence 3, Appli
2	1155.5	99.1	230	21	US-09-724-676-83309	Sequence 83309, A
3	1155.5	99.1	230	21	US-09-724-676A-83309	Sequence 83309, A
4	1155.5	99.1	288	33	US-60-452-680-22670	Sequence 22670, A
5	1155.5	99.1	349	22	US-09-791-537-37838	Sequence 37838, A
6	1155.5	99.1	349	22	US-60-452-680-22672	Sequence 22672, A
7	1155.5	99.1	376	33	US-60-452-680-22671	Sequence 22671, A
8	1155.5	99.1	426	21	US-09-724-676-83308	Sequence 83308, A
9	1155.5	99.1	426	21	US-09-724-676A-83308	Sequence 83308, A
10	1155.5	99.1	622	1	PCT-US01-49049-3	Sequence 3, Appli
11	1155.5	99.1	622	1	PCT-US01-49049A-3	Sequence 3, Appli
12	1155.5	99.1	622	1	PCT-US02-19669-373	Sequence 373, App
13	1155.5	99.1	622	1	PCT-US02-19669A-373	Sequence 373, App
14	1155.5	99.1	622	22	US-09-791-537-18829	Sequence 18829, A
15	1155.5	99.1	622	26	US-10-058-270A-40	Sequence 40, Appl
16	1155.5	99.1	622	27	US-10-177-293-373	Sequence 373, App
17	1155.5	99.1	622	28	US-10-395-027-112	Sequence 112, App
18	1155.5	99.1	622	28	US-10-395-027-744	Sequence 744, App
19	1155.5	99.1	622	33	US-60-452-680-22669	Sequence 22669, A
20	1155.5	99.1	637	24	US-09-949-016-10128	Sequence 10128, A
21	1052.5	99.3	622	22	US-09-791-537-3751	Sequence 3751, Ap
22	1036.5	88.9	206	22	US-09-791-537-24513	Sequence 24513, A
23	1036.5	88.9	211	7	US-08-310-552-2	Sequence 2, Appli
24	1036.5	88.9	211	22	US-09-791-537-116008	Sequence 116008, A
25	987	84.6	597	28	US-10-287-971-74	Sequence 74, Appl
26	935.5	80.2	616	22	US-09-791-537-99548	Sequence 99548, A
27	901.5	77.3	581	22	US-09-791-537-119333	Sequence 119333, A
28	888.5	76.2	625	22	US-09-791-537-23820	Sequence 23820, A
29	865.5	74.2	296	22	US-09-791-537-53150	Sequence 53150, A
30	865.5	74.2	581	22	US-09-791-537-119332	Sequence 119332, A
31	863.5	74.1	296	22	US-09-791-537-107221	Sequence 107221, A
32	863.5	74.1	581	22	US-09-791-537-36028	Sequence 36028, A
33	837	71.8	310	22	US-09-791-537-85473	Sequence 85473, A
34	837	71.8	412	22	US-09-791-537-93032	Sequence 93032, A
35	813.5	69.8	292	22	US-09-791-537-62081	Sequence 62081, A
36	813.5	69.8	303	22	US-09-791-537-62063	Sequence 62063, A
37	813.5	69.8	608	22	US-09-791-537-35679	Sequence 35679, A
38	813.5	69.8	608	22	US-09-791-537-64104	Sequence 64104, A
39	799.5	68.6	210	22	US-09-791-537-86333	Sequence 86333, A
40	764.5	65.6	198	22	US-09-791-537-95162	Sequence 95162, A
41	688.5	59.0	831	22	US-09-791-537-49689	Sequence 49689, A
42	683.5	58.6	217	22	US-09-791-537-96201	Sequence 96201, A
43	683.5	58.6	830	22	US-09-791-537-119338	Sequence 119338, A
44	682	58.5	831	22	US-09-791-537-119339	Sequence 119339, A
45	679	58.2	134	12	US-08-806-597-8	Sequence 8, Appli

## ALIGNMENTS

RESULT 1  
US-10-029-079-3  
; Sequence 3, Application US/10029079  
; GENERAL INFORMATION:  
; APPLICANT: Clevenger, Charles V  
; APPLICANT: Kline, J. Bradford  
; TITLE OF INVENTION: Composition and Method for Modulating Somatolactogenic Function  
; FILE REFERENCE: PENN-0795  
; CURRENT APPLICATION NUMBER: US/10/029,079  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: 60/258,285  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 3  
; LENGTH: 210  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-029-079-3

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Best Local Similarity 100.0%; Pred.No. 3.6e-118;  
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Best Local Similarity 99.5%; Pred. No. 5.7e-117;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMMRTYIMMNVAT-QMGSSFSDELYVD 120  
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMMRTYIMMNVAT-QMGSSFSDELYVD 120  
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DB 121 TYIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYIRLKPKEAAEW 180  
QY 181 IHFAGQOTEFKILSLHPGQKYLQVRCRCPD 210  
DB 181 IHFAGQOTEFKILSLHPGQKYLQVRCRCPD 210

## RESULT 2

US-09-724-676-83309

; Sequence 83309, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 83309  
; LENGTH: 230  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676-83309

Query Match 99.1%; Score 1155.5; DB 21; Length 230;  
Best Local Similarity 99.5%; Pred. No. 5.7e-117;  
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QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMMRTYIMMNVAT-QMGSSFSDELYVD 119  
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMMRTYIMMNVAT-QMGSSFSDELYVD 120  
QY 120 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYIRLKPKEAAEW 179  
DB 121 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYIRLKPKEAAEW 180  
QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 210  
DB 181 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 211

## RESULT 3

US-09-724-676A-83309

; Sequence 83309, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 83309  
; LENGTH: 230  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676A-83309

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DB 121 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYIRLKPKEAAEW 180  
QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 210  
DB 181 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 211

## RESULT 4

US-60-452-680-22670

; Sequence 22670, Application US/60452680  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; APPLICANT: GRUPE, Andrew  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001450  
; CURRENT APPLICATION NUMBER: US/60/452,680  
; CURRENT FILING DATE: 2003-03-07  
; NUMBER OF SEQ ID NOS: 116213  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22670  
; LENGTH: 288  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-60-452-680-22670

Query Match 99.1%; Score 1155.5; DB 33; Length 288;  
Best Local Similarity 99.5%; Pred. No. 7.7e-117;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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QY 120 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYIRLKPKEAAEW 179  
DB 121 VTIVQDPDPPELEAVEVKQPEDRKPYLWKSPPTLIDLTGFTLLYIRLKPKEAAEW 180  
QY 180 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 210  
DB 181 EHFAGQOTEFKILSLHPGQKYLQVRCRCPD 211

## RESULT 5

US-09-791-537-37838

; Sequence 37838, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22



; NUMBER OF SEQ ID NOS: 153055  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 37838  
 ; LENGTH: 349  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-791-537-37838

Query Match 99.1%; Score 1155.5; DB 22; Length 349;  
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 DB 121 VTYIVQDPDPLEAVEVKQEDRPKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 180  
 QY 180 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 210  
 DB 181 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 6

US-60-452-680-22672  
 ; Sequence 22672, Application US/60452680

; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001450  
 ; CURRENT APPLICATION NUMBER: US/60/452,680  
 ; CURRENT FILING DATE: 2003-03-07  
 ; NUMBER OF SEQ ID NOS: 116213  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 22672  
 ; LENGTH: 349  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-452-680-22672

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 Best Local Similarity 99.5%; Pred. No. 1e-116;  
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 DB 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 120  
 QY 120 VTYIVQDPDPLEAVEVKQEDRPKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 179  
 DB 121 VTYIVQDPDPLEAVEVKQEDRPKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 180  
 QY 180 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 210  
 DB 181 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 7

US-60-452-680-22671  
 ; Sequence 22671, Application US/60452680  
 ; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele  
 ; APPLICANT: GROUPE, Andrew  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001450  
 ; CURRENT APPLICATION NUMBER: US/60/452,680  
 ; CURRENT FILING DATE: 2003-03-07  
 ; NUMBER OF SEQ ID NOS: 116213  
 ; SOFTWARE: Fast-Seq for Windows Version 4.0  
 ; SEQ ID NO 22671  
 ; LENGTH: 376  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-60-452-680-22671

Query Match 99.1%; Score 1155.5; DB 33; Length 376;  
 Best Local Similarity 99.5%; Pred. No. 1e-116;  
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 DB 121 VTYIVQDPDPLEAVEVKQEDRPKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 180  
 QY 180 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 210  
 DB 181 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 8

US-09-724-676-83308  
 ; Sequence 83308, Application US/09724676

; GENERAL INFORMATION:

; APPLICANT: Compugen LTD  
 ; TITLE OF INVENTION: Variants of alternative splicing  
 ; FILE REFERENCE: 129181.4 Compugen  
 ; CURRENT APPLICATION NUMBER: US/09/724,676  
 ; CURRENT FILING DATE: 2000-11-28  
 ; NUMBER OF SEQ ID NOS: 97222  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 83308  
 ; LENGTH: 426  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-724-676-83308

Query Match 99.1%; Score 1155.5; DB 21; Length 426;  
 Best Local Similarity 99.5%; Pred. No. 1.3e-116;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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 QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 119  
 DB 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 120  
 QY 120 VTYIVQDPDPLEAVEVKQEDRPKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 179  
 DB 121 VTYIVQDPDPLEAVEVKQEDRPKPYLWKSPPTLIDLTGWTLLYEIRLKPEKAAEW 180  
 QY 180 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 210  
 DB 181 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 211

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RESULT 9
US-09-724-676A-83308
; Sequence 83308, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83308
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-49049-3
; Sequence 3, Application PC/TUS0149049
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bieglecki, Karyn M
; APPLICANT: Duda, Amy
; APPLICANT: Koshv, Beena
; TITLE OF INVENTION: HAPLOTYPES OF THE PRLR GENE
; FILE REFERENCE: PRLR_MWH-0892PCT
; CURRENT APPLICATION NUMBER: PCT/US01/49049A
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,523
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-49049A-3
Query Match 99.1%; Score 1155.5; DB 1; Length 426;
Best Local Similarity 99.5%; Pred. No. 1.2e-116;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60
DB 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWRTYIMMVNAT-QMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWRTYIMMVNAT-QMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYRILKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYRILKPEKAAEW 180
QY 180 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 210
DB 181 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 211
RESULT 10
PCT-US01-49049-3
; Sequence 3, Application PC/TUS0149049
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bieglecki, Karyn M
; APPLICANT: Duda, Amy
; APPLICANT: Koshv, Beena
; TITLE OF INVENTION: HAPLOTYPES OF THE PRLR GENE
; FILE REFERENCE: PRLR_MWH-0892PCT
; CURRENT APPLICATION NUMBER: PCT/US01/49049
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,523
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-49049-3
Query Match 99.1%; Score 1155.5; DB 1; Length 622;
Best Local Similarity 99.5%; Pred. No. 2.2e-116;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60
DB 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWRTYIMMVNAT-QMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWRTYIMMVNAT-QMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYRILKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYRILKPEKAAEW 180
QY 180 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 210
DB 181 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 211
RESULT 11
PCT-US01-49049A-3
; Sequence 3, Application PC/TUS0149049A
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bieglecki, Karyn M
; APPLICANT: Duda, Amy
; APPLICANT: Koshv, Beena
; TITLE OF INVENTION: HAPLOTYPES OF THE PRLR GENE
; FILE REFERENCE: PRLR_MWH-0892PCT
; CURRENT APPLICATION NUMBER: PCT/US01/49049A
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,523
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-49049A-3
Query Match 99.1%; Score 1155.5; DB 1; Length 622;
Best Local Similarity 99.5%; Pred. No. 2.2e-116;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60
DB 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWRTYIMMVNAT-QMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMTWRTYIMMVNAT-QMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYRILKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYRILKPEKAAEW 180
QY 180 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 210
DB 181 EHFAGQQTTEFKILSLHPGQKYLQVVRCKPD 211
RESULT 12
PCT-US02-19669-373
; Sequence 373, Application PC/TUS0219669
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038FC
; CURRENT APPLICATION NUMBER: PCT/US02/19669
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
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; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-19669-373

Query Match          99.1%; Score 1155.5; DB 1; Length 622;
Best Local Similarity 99.5%; Pred. No. 2.2e-116;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
QY 61 SLTYHREGETLMHCEPDYITGGPNSCHFGKQYTSWRTYIMVYNAT-QMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHCEPDYITGGPNSCHFGKQYTSWRTYIMVYNATQMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGTWFTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGTWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFAGQOTFEKILSLHFGQKYLQVVRCKPD 210
DB 181 EIHFAGQOTFEKILSLHFGQKYLQVVRCKPD 211

RESULT 13
PCT-US02-19669A-373
; Sequence 373, Application PC/TUS0219669A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038PC
; CURRENT APPLICATION NUMBER: PCT/US02/19669A
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-19669A-373

Query Match          99.1%; Score 1155.5; DB 1; Length 622;
Best Local Similarity 99.5%; Pred. No. 2.2e-116;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
QY 61 SLTYHREGETLMHCEPDYITGGPNSCHFGKQYTSWRTYIMVYNAT-QMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHCEPDYITGGPNSCHFGKQYTSWRTYIMVYNATQMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGTWFTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGTWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFAGQOTFEKILSLHFGQKYLQVVRCKPD 210
DB 181 EIHFAGQOTFEKILSLHFGQKYLQVVRCKPD 211

RESULT 14
US-09-791-537-18829
; Sequence 18829, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18829
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-18829

Query Match          99.1%; Score 1155.5; DB 22; Length 622;
Best Local Similarity 99.5%; Pred. No. 2.2e-116;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
DB 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
QY 61 SLTYHREGETLMHCEPDYITGGPNSCHFGKQYTSWRTYIMVYNAT-QMGSSFSDELYVD 119
DB 61 SLTYHREGETLMHCEPDYITGGPNSCHFGKQYTSWRTYIMVYNATQMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGTWFTLLYEIRLKPEKAAEW 179
DB 121 VTYIVQDPDPLEAVEVKQPEDRKPYLWKSPPTLIDLTGTWFTLLYEIRLKPEKAAEW 180
QY 180 EIHFAGQOTFEKILSLHFGQKYLQVVRCKPD 210
DB 181 EIHFAGQOTFEKILSLHFGQKYLQVVRCKPD 211

RESULT 15
US-10-058-270A-40
; Sequence 40, Application US/10058270A
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Afar, Daniel
; APPLICANT: Bos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Breast Cancer
; FILE REFERENCE: 018501-005210US
; CURRENT APPLICATION NUMBER: US/10/058,270A
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,965
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/265,928
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 09/829,472
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/282,698
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 60/288,590
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,443
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; PRIOR FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 141  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 40  
 ; LENGTH: 622  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-058-270A-40

Query Match 99.1%; Score 1155.5; DB 26; Length 622;  
 Best Local Similarity 99.5%; Pred. No. 2.2e-116;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 Qy 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 Db 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 Qy 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMMRTYIMVNAT-OMGSSFSDELYVD 119  
 Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMMRTYIMVNAT-OMGSSFSDELYVD 120  
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 Qy 180 EIHFAQOOTEFKILSLHPGOKYLVQVRCRDP 210  
 Db 181 EIHFAQOOTEFKILSLHPGOKYLVQVRCRDP 211

Search completed: May 12, 2004, 16:23:19  
 Job time : 184 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:18:01 ; Search time 20 Seconds  
(without alignments)  
365.723 Million cell updates/sec

Title: US-10-029-079-3  
Perfect score: 1166  
Sequence: 1 MKENVASATVFILLFLNTC.....KILSLHPGQKYLVRCKPD 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 235879 seqs, 34830801 residues

Total number of hits satisfying chosen parameters: 235879

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA New:\*  
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2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
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7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	293	25.1	410	US-10-778-002-12	Sequence 12, Appl
2	293	25.1	422	US-10-821-801-794	Sequence 794, Appl
3	292	25.0	405	US-09-736-842-2	Sequence 2, Appl
4	292	25.0	407	US-10-778-002-13	Sequence 13, Appl
5	292	25.0	425	US-10-603-151-2	Sequence 2, Appl
6	273	23.4	434	US-09-736-842-4	Sequence 4, Appl
7	273	23.4	448	US-09-736-842-6	Sequence 6, Appl
8	262.5	22.5	202	US-10-806-655-4	Sequence 4, Appl
9	262.5	22.5	203	US-10-806-655-3	Sequence 3, Appl
10	262.5	22.5	206	US-10-806-655-2	Sequence 2, Appl
11	262.5	22.5	237	US-10-806-655-1	Sequence 1, Appl
12	262.5	22.5	638	PCT-US04-02188-142	Sequence 142, App
13	262.5	22.5	638	US-10-764-425-142	Sequence 142, App
14	262.5	22.5	638	US-10-821-801-503	Sequence 503, App
15	190.5	16.3	837	US-10-659-295-35	Sequence 35, Appl
16	165	14.2	918	US-10-667-290-3	Sequence 3, Appl
17	165	14.2	918	US-10-667-289-3	Sequence 3, Appl
18	163	14.0	836	US-10-659-295-34	Sequence 34, Appl
19	163	14.0	836	US-10-821-234-1559	Sequence 1559, Ap
20	161	13.8	379	US-10-779-890-11	Sequence 11, Appl
21	153	13.1	422	PCT-US04-02188-137	Sequence 137, App
22	153	13.1	422	US-10-764-425-137	Sequence 137, App
23	126	10.8	378	US/09/077	Sequence 12, Appl
24	126	10.8	380	US-09-077-817D-2	Sequence 2, Appl
25	125	10.7	662	US-10-772-531-54	Sequence 54, Appl
26	125	10.7	764	US-10-772-531-69	Sequence 69, Appl

27 122 10.5 239 6 US-10-772-531-22 Sequence 22, Appl  
28 122 10.5 324 6 US-10-772-531-18 Sequence 18, Appl  
29 122 10.5 649 6 US-10-772-531-46 Sequence 46, Appl  
30 122 10.5 732 6 US-10-772-531-2 Sequence 2, Appl  
31 114 9.8 1204 6 US-10-712-124-100 Sequence 100, App  
32 113.5 9.7 427 5 US-09-077-817D-4 Sequence 4, Appl  
33 111.5 9.6 1518 1 PCT-US04-07412-580 Sequence 580, App  
34 110 9.4 229 6 US-10-777-790-10 Sequence 10, Appl  
35 108.5 9.3 547 6 US-10-772-531-93 Sequence 93, Appl  
36 108.5 9.3 662 6 US-10-772-531-57 Sequence 57, Appl  
37 108.5 9.3 906 7 US-60-548-091-413 Sequence 413, App  
38 108.5 9.3 958 7 US-60-548-091-414 Sequence 414, App  
39 108.5 9.3 1165 7 US-60-548-091-412 Sequence 412, App  
40 108.5 9.3 1165 7 US-60-548-091-415 Sequence 415, App  
41 103.5 8.9 862 6 US-10-667-280-4 Sequence 4, Appl  
42 103.5 8.9 862 6 US-10-667-289-4 Sequence 4, Appl  
43 103.5 8.9 862 6 US-10-797-157-7 Sequence 7, Appl  
44 103.5 8.9 862 6 US-10-370-715B-68 Sequence 68, Appl  
45 102.5 8.8 507 1 PCT-US04-09416-2 Sequence 2, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-778-002-12  
; Sequence 12, Application US/10778002  
; GENERAL INFORMATION:  
; APPLICANT: Oppmann, Birgit  
; APPLICANT: Timans, Jacqueline C.  
; APPLICANT: Kastelein, Robert A.  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; FILE REFERENCE: DX0935K  
; CURRENT APPLICATION NUMBER: US/10/778,002  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/09/521,335  
; PRIOR FILING DATE: 2000-03-09  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: primate  
US-10-778-002-12

Query Match 25.1%; Score 293; DB 6; Length 410;  
Best Local Similarity 37.5%; Pred. No. 3.5e-20;  
Matches 75; Conservative 28; Mismatches 85; Indels 12; Gaps 8;  
QY 15 LFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGG--LPTNYSLYHREGETLM 72  
Db 123 ILAGSCLYVG-LPPEKPVNISCWSKMKDLACRWTPGAHGETFLHTNYSLYKLRWYQDD 181  
QY 73 HECPDYITGGNSCHFGKQYTSMTWTYIMYNAT--CMGSSPSDELYVDVTIVQDPDPLE 131  
Db 182 NTCEYHTVGHPSCHIPKD-LALFTPYEIVWEATNRLGARSADVLTLLDVTVDTPPD 240  
QY 132 LAV-EVKQPEDEKPKYLWIKWSPPPTLIDLKGTWFTLLYELRLKPEKAAEWE-IHFAGQOTE 189  
Db 241 VHVSRVGGLEDQLSVRWV--SPPALKDF--LFAQKYQIRVRVEDSVDMKVVDVSNQTS 295  
QY 190 FKLSLHPGQKYLVRCKP 209  
Db 296 CRLAGLKPGTVFVQVRCNP 315

##### RESULT 2

US-10-821-801-794  
; Sequence 794, Application US/10821801  
; GENERAL INFORMATION:  
; APPLICANT: Hinzmann, Bernd  
; APPLICANT: Rosenthal, Andre

```

; APPLICANT: Hermann, Klaus
; APPLICANT: Heiden, Esmeralda
; APPLICANT: Pilarzsky, Christian
; APPLICANT: Brummendorf, Thomas
; APPLICANT: Staub, Eike
; APPLICANT: Ropcke, Stefan
; APPLICANT: Mennerich, Detlev
; APPLICANT: Kinnemann, Henrik
; APPLICANT: Li, Xinzhang
; TITLE OF INVENTION: Human nucleic acid sequences from lung tumours
; FILE REFERENCE: 00154/002001
; CURRENT APPLICATION NUMBER: US/10/821,801
; CURRENT FILING DATE: 2004-04-09
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 794
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-821-801-794

Query Match      25.1%; Score 293; DB 6; Length 422;
Best Local Similarity 37.5%; Pred. No. 3.6e-20;
Matches 75; Conservative 28; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKTFTCWRPGTDGG--LPTNYSLTYYHREGETLM 72
DB 123 ILAGSLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGD 181
QY 73 HECPDYITGGPNSCHFGKQVTSWRTYIMVNAT-QMGSSFSDELYVDVTVIYQDPDPLE 131
DB 182 NTCEEYHTVGPCHSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPPD 240
QY 132 LAV-EVKQPEDRKPYLWKSPPTLIDLTGTFLLYEIRLKEPKAAEWE-IHFAGQOOTE 189
DB 241 VHVSRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVSDSVDMKVVDDVSNQTS 295
QY 190 FKILSLHPGQKYLVOVRCKP 209
DB 296 CRLAGLKPGETVYFVQVRCP 315

RESULT 3
US-09-736-842-2
; Sequence 2, Application US/09736842
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: Novel Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/736,842
; CURRENT FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US/09/120,601
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/012,072
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-736-842-2

Query Match      25.0%; Score 292; DB 5; Length 405;
Best Local Similarity 38.0%; Pred. No. 4.3e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

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DB 106 ILAGSLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGD 164

RESULT 4
US-10-778-002-13
; Sequence 13, Application US/10778002
; GENERAL INFORMATION:
; APPLICANT: Oppmann, Birgit
; APPLICANT: Ilmans, Jacqueline C.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
; FILE REFERENCE: DX0935K
; CURRENT APPLICATION NUMBER: US/10/778,002
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US/09/521,335
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 407
; TYPE: PRT
; ORGANISM: rodent
US-10-778-002-13

Query Match      25.0%; Score 292; DB 6; Length 407;
Best Local Similarity 38.0%; Pred. No. 4.3e-20;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKTFTCWRPGTDGG--LPTNYSLTYYHREGETLM 72
DB 108 ILAGSLYVG-LPPEKPFNISCWSRNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYGD 166
QY 73 HECPDYITGGPNSCHFGKQVTSWRTYIMVNAT-QMGSSFSDELYVDVTVIYQDPDPLE 131
DB 167 NTCEEYHTVGPCHSCHIPKD-LALFTPYEIVWEATNRLGARSVDLTLDVLDVTTDPPD 225
QY 132 LAV-EVKQPEDRKPYLWKSPPTLIDLTGTFLLYEIRLKEPKAAEWE-IHFAGQOOTE 189
DB 226 VHVSRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVSDSVDMKVVDDVSNQTS 280
QY 190 FKILSLHPGQKYLVOVRCKP 209
DB 281 CRLAGLKPGETVYFVQVRCP 300

RESULT 5
US-10-603-151-2
; Sequence 2, Application US/10603151
; GENERAL INFORMATION:
; APPLICANT: Keith D. Allen
; TITLE OF INVENTION: CRFL1 Gene Disruptions, Compositions and Methods Related Thereto
; FILE REFERENCE: R-344
; CURRENT APPLICATION NUMBER: US/10/603,151
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US 60/391,170
; PRIOR FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT

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; ORGANISM: Mus musculus
US-10-603-151-2

Query Match
Best Local Similarity 25.0%; Score 292; DB 6; Length 425;
Matches 76; Conservative 27; Mismatches 85; Indels 12; Gaps 8;

QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKEFTTCWRPFGTDGG--LPTNYSILTYHREGETLM 72
DB 126 ILAGSCLYVG-LPPEKPNISCSNRNKKDLTCRTWTFGAHGETFLHTNYSILKYKLRWYQD 184
QY 73 HECPDYITGPNNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVDVYIVQDDPLE 131
DB 185 NTCEEYHTVGPCHSCHKD-LALFTPEIWEATNRLGARSVDLTLDVLDVYVTTDPPD 243
QY 132 LAV-EVKQEDRKPYLWIKWSPTLIDLTGFTLLYEIRLKEPKAAWE-IHFAGQOTE 189
DB 244 VHVSRVGGLEDQLSVRWV--SPALKDF---LFQAKYQIRYVEDSVDMKVVDDVSNQTS 298
QY 190 FKILSLHPGQKYLQVQRCKP 209
DB 299 CRLAGLKPGTVYFVQVRCNP 318

RESULT 6
US-09-736-842-4
; Sequence 4, Application US/09736842
; GENERAL INFORMATION:
; APPLICANT: Maslakowski, Piotr
; TITLE OF INVENTION: Novel Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/736,842
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US/09/120,601
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/012,072
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 434
; TYPE: PRT
; ORGANISM: HUMAN
US-09-736-842-4

Query Match
Best Local Similarity 23.4%; Score 273; DB 5; Length 434;
Matches 75; Conservative 28; Mismatches 85; Indels 34; Gaps 9;

QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKEFTTCWRPFGTDGG--LPTNYSILTYHREGETLM 72
DB 109 ILAGSCLYVG-LPPEKPNISCSNRNKKDLTCRTWTFGAHGETFLHTNYSILKYKLRWYQD 167
QY 73 HECPDYITGPNNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVDVYIVQDDPLE 121
DB 168 NTCEEYHTVGPCHSCHKD-LALFTPEIWEATNRLGARSVDLTLDVLDVYVTTDPPD 226
QY 122 -----YIVQDDPLELAV-EVKQEDRKPYLWIKWSPTLIDLTGFTLLYEIRLKEPKAAWE-IHFAGQOTE 168
DB 227 PATPGLSLLVRGKVYVTTDPPDPPDVHVSRVGGLEDQLSVRWV--SPALKDF---LFQAKYQ 281
QY 169 IRLKPEKAAWE-IHFAGQOTEFKILSLHPGQKYLQVQRCKP 209
DB 282 IRYVEDSVDMKVVDDVSNQTSRLAGLKPGTVYFVQVRCNP 323

RESULT 7
US-09-736-842-6
; Sequence 6, Application US/09736842
; GENERAL INFORMATION:
; APPLICANT: Maslakowski, Piotr
; TITLE OF INVENTION: Novel Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/736,842
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US/09/120,601
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/012,072
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 448
; TYPE: PRT
; ORGANISM: HUMAN
US-09-736-842-6

Query Match
Best Local Similarity 23.4%; Score 273; DB 5; Length 448;
Matches 75; Conservative 28; Mismatches 85; Indels 34; Gaps 9;

QY 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKEFTTCWRPFGTDGG--LPTNYSILTYHREGETLM 72
DB 123 ILAGSCLYVG-LPPEKPNISCSNRNKKDLTCRTWTFGAHGETFLHTNYSILKYKLRWYQD 181
QY 73 HECPDYITGPNNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVDVYIVQDDPLE 121
DB 182 NTCEEYHTVGPCHSCHKD-LALFTPEIWEATNRLGARSVDLTLDVLDVYVTTDPPD 240
QY 122 -----YIVQDDPLELAV-EVKQEDRKPYLWIKWSPTLIDLTGFTLLYEIRLKEPKAAWE-IHFAGQOTE 168
DB 241 PATPGLSLLVRGKVYVTTDPPDPPDVHVSRVGGLEDQLSVRWV--SPALKDF---LFQAKYQ 295
QY 169 IRLKPEKAAWE-IHFAGQOTEFKILSLHPGQKYLQVQRCKP 209
DB 296 IRYVEDSVDMKVVDDVSNQTSRLAGLKPGTVYFVQVRCNP 337

RESULT 8
US-10-806-655-4
; Sequence 4, Application US/10806655
; GENERAL INFORMATION:
; APPLICANT: Sundstrom, Michael
; TITLE OF INVENTION: Modified Cytokine Receptor Protein
; FILE REFERENCE: 31611-8A
; CURRENT APPLICATION NUMBER: US/10/806,655
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US 09/355664
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: PCT/SE98/00277
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: SE 9700566 4
; PRIOR FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-806-655-4

Query Match
Best Local Similarity 22.5%; Score 262.5; DB 6; Length 202;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKEFTTCWRV---RPGTD--GGLPNTNYSILTYHREGETLMHECPDYITGCP 83
DB 19 EPKFTKCRSPERETFSCHWTDEVHGTGKVLGFIQLFYTRNTQEWTKMKECPDYVSAGE 78
QY 84 NSCHFGKQYTSWRTYIMVNATOMGSSFSDELYVDVYIVQDDPLELAVEVQKPEDRK 143
DB 79 NSCYNSSFSTSIWIPY--CIKLTSSNGGTV-DEKCFSDVEIVQDDPIALN----- 125
QY 144 PYLW-----IKWSPPTLIDLTGFTLLYEIRLKEPKAAWEIHFAGQOT 188
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Db 126 ---WTLNVLSTGIHADIQVRWEAPRNADIQKGMVLEVELOQYKEVNETKWKMDPILTT 182
QY 189 EFKILSLHPGQKYLIVQVRCK 208
Db 183 SVPVYSLKVDKEYEVRVRSK 202

RESULT 9
US-10-806-655-3
; Sequence 3, Application US/10806655
; GENERAL INFORMATION:
; APPLICANT: Sundstrom, Michael
; APPLICANT: Norstedt, Gunnar
; TITLE OF INVENTION: Modified Cytokine Receptor Protein
; FILE REFERENCE: 31611-8A
; CURRENT APPLICATION NUMBER: US/10/806,655
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US 09/355664
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: PCT/SE98/00277
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: SE 9700566 4
; PRIOR FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-806-655-3

Query Match 22.5%; Score 262.5; DB 6; Length 203;
Best Local Similarity 31.0%; Pred. No. 1.2e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKETFTCW----RPGTD--GGLPNTYSLTYHREGTLMHCEPDYITGGP 83
Db 19 EPKFTKCRSPERETFSCHWTDEVHHGTKNLGPIQLFYTRNTQEWTKQWKECPDYVSAGE 78
QY 84 NSCHFGQYTSWVRTYIMMNVNATQMGSSFSDELVDVTVIVQDPPLLEAVEVKQPEDRK 143
Db 79 NSCYFNSFTSIWIPY--CIKLTNSGGTV-DEKCFSDVEIVQDPPIALN-----125
QY 144 PYLW-----IKWSPPTLIDLTGNTFTLLYEIRLKPKEAAWEIHFAGQQT 188
Db 126 ---WTLNVLSTGIHADIQVRWEAPRNADIQKGMVLEVELOQYKEVNETKWKMDPILTT 182
QY 189 EFKILSLHPGQKYLIVQVRCK 208
Db 183 SVPVYSLKVDKEYEVRVRSK 202

US-10-806-655-1
; Sequence 1, Application US/10806655
; GENERAL INFORMATION:
; APPLICANT: Sundstrom, Michael
; APPLICANT: Norstedt, Gunnar
; TITLE OF INVENTION: Modified Cytokine Receptor Protein
; FILE REFERENCE: 31611-8A
; CURRENT APPLICATION NUMBER: US/10/806,655
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US 09/355664
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: PCT/SE98/00277
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: SE 9700566 4
; PRIOR FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-806-655-1

Query Match 22.5%; Score 262.5; DB 6; Length 237;
Best Local Similarity 31.0%; Pred. No. 1.5e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKETFTCW----RPGTD--GGLPNTYSLTYHREGTLMHCEPDYITGGP 83
Db 50 EPKFTKCRSPERETFSCHWTDEVHHGTKNLGPIQLFYTRNTQEWTKQWKECPDYVSAGE 109
QY 84 NSCHFGQYTSWVRTYIMMNVNATQMGSSFSDELVDVTVIVQDPPLLEAVEVKQPEDRK 143
Db 110 NSCYFNSFTSIWIPY--CIKLTNSGGTV-DEKCFSDVEIVQDPPIALN-----156
QY 144 PYLW-----IKWSPPTLIDLTGNTFTLLYEIRLKPKEAAWEIHFAGQQT 188
Db 157 ---WTLNVLSTGIHADIQVRWEAPRNADIQKGMVLEVELOQYKEVNETKWKMDPILTT 213
QY 189 EFKILSLHPGQKYLIVQVRCK 208
Db 214 SVPVYSLKVDKEYEVRVRSK 233

RESULT 12
PCT-US04-02188-142
; Sequence 142, Application PC/TUS0402188
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-806-655-2

Query Match 22.5%; Score 262.5; DB 6; Length 206;
Best Local Similarity 31.0%; Pred. No. 1.2e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKETFTCW----RPGTD--GGLPNTYSLTYHREGTLMHCEPDYITGGP 83
Db 19 EPKFTKCRSPERETFSCHWTDEVHHGTKNLGPIQLFYTRNTQEWTKQWKECPDYVSAGE 78
QY 84 NSCHFGQYTSWVRTYIMMNVNATQMGSSFSDELVDVTVIVQDPPLLEAVEVKQPEDRK 143
Db 79 NSCYFNSFTSIWIPY--CIKLTNSGGTV-DEKCFSDVEIVQDPPIALN-----125
QY 144 PYLW-----IKWSPPTLIDLTGNTFTLLYEIRLKPKEAAWEIHFAGQQT 188
Db 126 ---WTLNVLSTGIHADIQVRWEAPRNADIQKGMVLEVELOQYKEVNETKWKMDPILTT 182
QY 189 EFKILSLHPGQKYLIVQVRCK 208
Db 183 SVPVYSLKVDKEYEVRVRSK 202

RESULT 11
US-10-806-655-1
; Sequence 1, Application US/10806655
; GENERAL INFORMATION:
; APPLICANT: Sundstrom, Michael
; APPLICANT: Norstedt, Gunnar
; TITLE OF INVENTION: Modified Cytokine Receptor Protein
; FILE REFERENCE: 31611-8A
; CURRENT APPLICATION NUMBER: US/10/806,655
; CURRENT FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: US 09/355664
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: PCT/SE98/00277
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: SE 9700566 4
; PRIOR FILING DATE: 1997-02-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-806-655-1

Query Match 22.5%; Score 262.5; DB 6; Length 237;
Best Local Similarity 31.0%; Pred. No. 1.5e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKETFTCW----RPGTD--GGLPNTYSLTYHREGTLMHCEPDYITGGP 83
Db 50 EPKFTKCRSPERETFSCHWTDEVHHGTKNLGPIQLFYTRNTQEWTKQWKECPDYVSAGE 109
QY 84 NSCHFGQYTSWVRTYIMMNVNATQMGSSFSDELVDVTVIVQDPPLLEAVEVKQPEDRK 143
Db 110 NSCYFNSFTSIWIPY--CIKLTNSGGTV-DEKCFSDVEIVQDPPIALN-----156
QY 144 PYLW-----IKWSPPTLIDLTGNTFTLLYEIRLKPKEAAWEIHFAGQQT 188
Db 157 ---WTLNVLSTGIHADIQVRWEAPRNADIQKGMVLEVELOQYKEVNETKWKMDPILTT 213
QY 189 EFKILSLHPGQKYLIVQVRCK 208
Db 214 SVPVYSLKVDKEYEVRVRSK 233

RESULT 12
PCT-US04-02188-142
; Sequence 142, Application PC/TUS0402188
; GENERAL INFORMATION:
```



```

; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: PCT/US04/02188
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 142
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-02188-142

Query Match      22.5%; Score 262.5; DB 1; Length 638;
Best Local Similarity 31.0%; Pred. No. 4.8e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKEFTTCW-----RPGTD--GGLPTNYSLYTHREGETLMHECPDYITGGP 83
Db 50 EPKFTKCRSPERETFSCHWTDEVHHGTXNLGPIQLFYTRRNTQEWTKWKECPDYVSAGE 109
QY 84 NSCHFQKQYTSMTWRTYIMVNATQMGSSFSDELYVDVTYIVQDPPELEAVEVKQPEDRK 143
Db 110 NSCYFNSSFTSIWIPY--CIKLTSNGGTV-DEKCFSDVEIVQDPPIALN----- 156
QY 144 PYLW-----IKWSPPTLIDLKTGFTLLYIRLKPKEAAEWEIHFAGQOT 188
Db 157 ---WTLNVS�TGIHADIQVRWEAPRNADIQKGMWVLELYQYKEVNETKWKMDPILTT 213
QY 189 EFKILSLHPGQKYLQVRCK 208
Db 214 SVPVYSLKVDKEYEVRVRSK 233

Query Match      22.5%; Score 262.5; DB 6; Length 638;
Best Local Similarity 31.0%; Pred. No. 4.8e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKEFTTCW-----RPGTD--GGLPTNYSLYTHREGETLMHECPDYITGGP 83
Db 50 EPKFTKCRSPERETFSCHWTDEVHHGTXNLGPIQLFYTRRNTQEWTKWKECPDYVSAGE 109
QY 84 NSCHFQKQYTSMTWRTYIMVNATQMGSSFSDELYVDVTYIVQDPPELEAVEVKQPEDRK 143
Db 110 NSCYFNSSFTSIWIPY--CIKLTSNGGTV-DEKCFSDVEIVQDPPIALN----- 156
QY 144 PYLW-----IKWSPPTLIDLKTGFTLLYIRLKPKEAAEWEIHFAGQOT 188
Db 157 ---WTLNVS�TGIHADIQVRWEAPRNADIQKGMWVLELYQYKEVNETKWKMDPILTT 213
QY 189 EFKILSLHPGQKYLQVRCK 208
Db 214 SVPVYSLKVDKEYEVRVRSK 233

Query Match      22.5%; Score 262.5; DB 6; Length 638;
Best Local Similarity 31.0%; Pred. No. 4.8e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKEFTTCW-----RPGTD--GGLPTNYSLYTHREGETLMHECPDYITGGP 83
Db 50 EPKFTKCRSPERETFSCHWTDEVHHGTXNLGPIQLFYTRRNTQEWTKWKECPDYVSAGE 109
QY 84 NSCHFQKQYTSMTWRTYIMVNATQMGSSFSDELYVDVTYIVQDPPELEAVEVKQPEDRK 143
Db 110 NSCYFNSSFTSIWIPY--CIKLTSNGGTV-DEKCFSDVEIVQDPPIALN----- 156
QY 144 PYLW-----IKWSPPTLIDLKTGFTLLYIRLKPKEAAEWEIHFAGQOT 188
Db 157 ---WTLNVS�TGIHADIQVRWEAPRNADIQKGMWVLELYQYKEVNETKWKMDPILTT 213
QY 189 EFKILSLHPGQKYLQVRCK 208
Db 214 SVPVYSLKVDKEYEVRVRSK 233

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144 PYLW-----IKWSPPTLIDLKTGFTLLYIRLKPKEAAEWEIHFAGQOT 188
157 ---WTLNVS�TGIHADIQVRWEAPRNADIQKGMWVLELYQYKEVNETKWKMDPILTT 213
189 EFKILSLHPGQKYLQVRCK 208
214 SVPVYSLKVDKEYEVRVRSK 233

RESULT 14
US-10-821-801-503
; Sequence 503, Application US/10821801
; GENERAL INFORMATION:
; APPLICANT: Hinzmann, Bernd
; APPLICANT: Rosenthal, Andre
; APPLICANT: Hermann, Klaus
; APPLICANT: Heiden, Esmeralda
; APPLICANT: Pilarsky, Christian
; APPLICANT: Brumendorf, Thomas
; APPLICANT: Staub, Elke
; APPLICANT: Ropcke, Stefan
; APPLICANT: Mennerich, Detlev
; APPLICANT: Kinnemann, Henrik
; APPLICANT: Li, Xinzhang
; TITLE OF INVENTION: Human nucleic acid sequences from lung tumours
; FILE REFERENCE: 00154/002001
; CURRENT APPLICATION NUMBER: US/10/821,801
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: DE 103 16 701.3
; PRIOR FILING DATE: 2003-04-09
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 503
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-821-801-503

Query Match      22.5%; Score 262.5; DB 6; Length 638;
Best Local Similarity 31.0%; Pred. No. 4.8e-17;
Matches 62; Conservative 28; Mismatches 73; Indels 37; Gaps 6;

QY 30 KPEIFKCRSPNKEFTTCW-----RPGTD--GGLPTNYSLYTHREGETLMHECPDYITGGP 83
Db 50 EPKFTKCRSPERETFSCHWTDEVHHGTXNLGPIQLFYTRRNTQEWTKWKECPDYVSAGE 109
QY 84 NSCHFQKQYTSMTWRTYIMVNATQMGSSFSDELYVDVTYIVQDPPELEAVEVKQPEDRK 143
Db 110 NSCYFNSSFTSIWIPY--CIKLTSNGGTV-DEKCFSDVEIVQDPPIALN----- 156
QY 144 PYLW-----IKWSPPTLIDLKTGFTLLYIRLKPKEAAEWEIHFAGQOT 188
Db 157 ---WTLNVS�TGIHADIQVRWEAPRNADIQKGMWVLELYQYKEVNETKWKMDPILTT 213
QY 189 EFKILSLHPGQKYLQVRCK 208
Db 214 SVPVYSLKVDKEYEVRVRSK 233

RESULT 15
US-10-659-295-35
; Sequence 35, Application US/10659295
; GENERAL INFORMATION:
; APPLICANT: SCHNEIDER, ARMIN
; APPLICANT: SCHAEBITZ, WOLF-RUEDIGER
; APPLICANT: KOLLMAR, RAINER
; APPLICANT: SCHWAB, STEFAN
; TITLE OF INVENTION: METHODS OF TREATING NEUROLOGICAL CONDITIONS WITH HEMATOPOIETIC G
; FILE REFERENCE: 229530US
; CURRENT APPLICATION NUMBER: US/10/659,295
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US/10/331,755

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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:15:21 ; Search time 20 seconds  
(without alignments)  
1010.011 Million cell updates/sec

Title: US-10-029-079-3

Perfect score: 1166  
Sequence: 1 MKENVASATVFTLLFLNTC.....KILSLHPGQKYLIVQRKPD 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1155.5	99.1	288	B59405	prolactin receptor
2	1155.5	99.1	376	A59405	prolactin receptor
3	1155.5	99.1	622	A40144	prolactin receptor
4	935.5	80.2	616	A30304	prolactin receptor
5	865.5	74.2	581	I45971	prolactin receptor
6	837	71.8	310	A29854	prolactin receptor
7	837	71.8	412	A41070	prolactin receptor
8	837	71.8	610	A34631	prolactin receptor
9	837	71.8	610	A36116	prolactin receptor
10	813.5	69.8	292	I77525	prolactin receptor
11	813.5	69.8	303	I77524	prolactin receptor
12	813.5	69.8	608	I53269	prolactin receptor
13	688.5	59.0	831	QJ01655	prolactin receptor
14	683.5	58.6	830	I50455	prolactin receptor
15	549.5	47.1	630	I51086	prolactin receptor
16	504.5	43.3	150	B34631	prolactin receptor
17	489	41.9	156	A32868	prolactin receptor
18	312	26.8	97	I57699	pseudo-prolactin r
19	296	25.4	608	I32823	somatotropin recep
20	291.5	25.0	279	B32985	somatotropin-bindi
21	291.5	25.0	638	A33505	somatotropin recep
22	290.5	24.9	638	I32136	somatotropin recep
23	289.5	24.8	638	B28176	somatotropin recep
24	278.5	23.9	634	S33339	somatotropin-bindi
25	277.5	23.8	677	S33608	somatotropin recep
26	262.5	22.5	638	A33991	somatotropin recep
27	190.5	16.3	837	A34898	granulocyte colony
28	165	14.2	918	A36337	membrane glycoprot
29	163	14.0	771	B38252	granulocyte colony

30 163 14.0 783 2 JH0329 granulocyte colony  
31 163 14.0 863 2 C38252 granulocyte colony  
32 160 13.7 432 2 I48343 interleukin-11 rec  
33 153 13.1 422 2 I37891 interleukin-11 rec  
34 142.5 12.2 51 2 I56840 prolactin receptor  
35 138 11.8 917 2 I49699 glycoprotein 130 -  
36 134.5 11.5 918 2 A44257 interleukin-6 sign  
37 134 11.5 372 1 UHHUCN ciliary neurotroph  
38 133 11.4 362 2 S60614 growth promoting a  
39 131 11.2 372 2 I58141 ciliary neurotroph  
40 130.5 11.2 348 2 JC7907 common cytokine re  
41 124 10.6 440 2 JLC144 interleukin-6 rece  
42 124 10.6 460 2 JLC145 interleukin-6 rece  
43 120 10.3 805 2 S68441 leptin receptor, s  
44 120 10.3 892 2 S68439 leptin receptor, s  
45 120 10.3 894 2 S68437 leptin receptor, s

#### ALIGNMENTS

##### RESULT 1

B59405  
prolactin receptor short form Sib precursor, breast cancer cells T-47D - human  
C:Species: Homo sapiens (man)  
C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Mar-2002  
C:Accession: B59405; B49400  
R:Hu, Z.Z.; Meng, J.; Durau, M.L., 2001  
J. Biol. Chem. 276, 41086-41094, 2001  
A:Title: Isolation and characterization of two novel forms of the human prolactin recep  
A:Reference number: A59405; MUID:21538812; PMID:11518703  
A:Accession: B59405  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-288 <HU>  
A:Cross-references: GB:AF214012; PIDN:AF214012.1  
R:Hu, Z.Z.  
Submitted to GenBank, December, 1999  
A:Reference number: A49400  
A:Accession: B49400  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-288 <HU2>  
A:Cross-references: GB:AF214012; PIDN:AF214012.1  
C:Comment: This is one of the short forms (Sia and Sib) of the human prolactin receptor  
ta-casein gene promoter activation, with Sib more effective than Sia. However, their li  
C:Genetics:  
A:Gene: GDB:PRLR  
A:Cross-references: GDB:I20315; OMIM:176761  
A:Map position: Sp13.3-Sp13.1  
C:Superfamily: cytokine receptor transmembrane protein  
C:Keywords: glycoprotein; signal sequence #status predicted <SIG>  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-288/Product: prolactin receptor, short form Sib #status predicted <MAT>  
F:36-221/Domain: cytokine receptor homology <CRS>  
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.1%; Score 1155.5; DB 2; Length 288;  
Best Local Similarity 99.5%; Pred. No. 4.3e-95;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGPTNY 60  
Db 1 MKENVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTGGPTNY 60  
QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQVTSMWRTYIMVNAT-QVGSFSFSDLYVD 119  
Db 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQVTSMWRTYIMVNAT-QVGSFSFSDLYVD 120  
QY 120 VTYIVQDPPELAVVEVKQPEDRKPYLWKWSPPYLIDLKTGWFTLLYIRLKPEKAAEW 179  
Db 121 VTYIVQDPPELAVVEVKQPEDRKPYLWKWSPPYLIDLKTGWFTLLYIRLKPEKAAEW 180

QY 180 EHFAGQQTFFKILSLHPGQKYLQVRCRKP 210  
 |||  
 Db 181 EHFAGQQTFFKILSLHPGQKYLQVRCRKP 211

## RESULT 2

A59405  
 A:Accession: A59405  
 A:Molecule type: mRNA  
 A:Residues: 1-376 <HUI>  
 A:Cross-references: GB:A59405; A49400  
 R:Hu, Z.Z.; Meng, J.; Dufau, M.L.  
 J. Biol. Chem. 276, 41086-41094, 2001  
 A:Title: Isolation and characterization of two novel forms of the human prolactin receptor  
 A:Reference number: A59405; MUID:21538812; PMID:11518703  
 A:Accession: A59405  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-376 <HUI>  
 A:Cross-references: GB:AF214012; PIDN:AF214012.1  
 R:Hu, Z.Z.  
 Submitted to GenBank, December, 1999

A:Reference number: A49400  
 A:Accession: A49400  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-376 <HUI>  
 A:Cross-references: GB:AF214012; PIDN:AF214012.1  
 C:Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor  
 eta-casein gene promoter activation, with S1a less effective than S1b. However, their li  
 ted COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expe  
 C:Genetics:  
 A:Gene: GDB:PRLR  
 A:Cross-references: GDB:120315; OMIM:176761  
 A:Map position: Sp13.3-5p13.1  
 C:Superfamily: cytokine receptor homology  
 C:Keywords: glycoprotein; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-376/Product: prolactin receptor, short form S1a #status predicted <MAT>  
 F:36-221/Domain: cytokine receptor homology <CRS>  
 F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.1%; Score 1155.5; DB 2; Length 376;  
 Best Local Similarity 99.5%; Pred. No. 5.8e-95;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLLQQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 |||  
 Db 1 MKNVASATVFTLLFLNTCLLQQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60

QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELIVD 119  
 |||  
 Db 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNATQMGSSFSDELIVD 120

QY 120 VTIYVQDPPLLEAVEKQPEDEKPKYLIWKWSPTLIDLTGTFLLYERLKPKEAAEW 179  
 |||  
 Db 121 VTIYVQDPPLLEAVEKQPEDEKPKYLIWKWSPTLIDLTGTFLLYERLKPKEAAEW 180

QY 180 EHFAGQQTFFKILSLHPGQKYLQVRCRKP 210  
 |||  
 Db 181 EHFAGQQTFFKILSLHPGQKYLQVRCRKP 211

## RESULT 3

A40144  
 A:Accession: A40144  
 A:Molecule type: mRNA  
 A:Residues: 1-622 <BOU>  
 A:Cross-references: GB:M31661; NID:G190361; PIDN:AAA60174.1; PID:G190362  
 R:Fuh, G.; Wells, J.A.  
 J. Biol. Chem. 270, 13133-13137, 1995  
 A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li  
 A:Reference number: A57018; MUID:95286597; PMID:7768908  
 A:Accession: A57018  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 25-228, 'AW' <RES>  
 A:Cross-references: GB:S78505; NID:G999114; PIDN:AA34470.1; PID:G999115  
 C:Genetics:  
 A:Gene: GDB:PRLR  
 A:Cross-references: GDB:120315; OMIM:176761  
 A:Map position: Sp13.3-5p13.1  
 C:Superfamily: cytokine receptor homology  
 C:Keywords: glycoprotein; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-622/Product: prolactin receptor, long form #status predicted <MAT>  
 F:36-221/Domain: cytokine receptor homology <CRS>  
 F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

A:Accession: A40144  
 A:Molecule type: mRNA  
 A:Residues: 1-622 <BOU>  
 A:Cross-references: GB:M31661; NID:G190361; PIDN:AAA60174.1; PID:G190362  
 R:Fuh, G.; Wells, J.A.  
 J. Biol. Chem. 270, 13133-13137, 1995  
 A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li  
 A:Reference number: A57018; MUID:95286597; PMID:7768908  
 A:Accession: A57018  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 25-228, 'AW' <RES>  
 A:Cross-references: GB:S78505; NID:G999114; PIDN:AA34470.1; PID:G999115  
 C:Genetics:  
 A:Gene: GDB:PRLR  
 A:Cross-references: GDB:120315; OMIM:176761  
 A:Map position: Sp13.3-5p13.1  
 C:Superfamily: cytokine receptor homology  
 C:Keywords: glycoprotein; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-622/Product: prolactin receptor, long form #status predicted <MAT>  
 F:36-221/Domain: cytokine receptor homology <CRS>  
 F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 99.1%; Score 1155.5; DB 2; Length 622;  
 Best Local Similarity 99.5%; Pred. No. 1e-94;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLLQQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 |||  
 Db 1 MKNVASATVFTLLFLNTCLLQQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60

QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELIVD 119  
 |||  
 Db 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNATQMGSSFSDELIVD 120

QY 120 VTIYVQDPPLLEAVEKQPEDEKPKYLIWKWSPTLIDLTGTFLLYERLKPKEAAEW 179  
 |||  
 Db 121 VTIYVQDPPLLEAVEKQPEDEKPKYLIWKWSPTLIDLTGTFLLYERLKPKEAAEW 180

QY 180 EHFAGQQTFFKILSLHPGQKYLQVRCRKP 210  
 |||  
 Db 181 EHFAGQQTFFKILSLHPGQKYLQVRCRKP 211

RESULT 4  
 A30304  
 A:Accession: A30304  
 A:Molecule type: mRNA  
 A:Residues: 1-616 <EDE>  
 A:Cross-references: GB:J04510; NID:G165669; PIDN:AAA31457.1; PID:G165670  
 R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.  
 Int. J. Biochem. 22, 1089-1095, 1990  
 A:Title: Purification and partial sequence of the rabbit mammary gland prolactin recepto  
 A:Reference number: A60380; MUID:91146782; PMID:2289615  
 A:Accession: A60380  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 41-58, 'X', 60-66, 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX', 167  
 A:Note: the amino end of the mature protein was blocked  
 C:Superfamily: cytokine receptor homology  
 C:Keywords: blocked amino end; glycoprotein; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-616/Product: prolactin receptor 2 #status predicted <MAT>  
 F:36-221/Domain: cytokine receptor homology <CRS>

Query Match 99.1%; Score 1155.5; DB 2; Length 376;  
 Best Local Similarity 99.5%; Pred. No. 5.8e-95;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLLQQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 |||  
 Db 1 MKNVASATVFTLLFLNTCLLQQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60

QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELIVD 119  
 |||  
 Db 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNATQMGSSFSDELIVD 120

QY 120 VTIYVQDPPLLEAVEKQPEDEKPKYLIWKWSPTLIDLTGTFLLYERLKPKEAAEW 179  
 |||  
 Db 121 VTIYVQDPPLLEAVEKQPEDEKPKYLIWKWSPTLIDLTGTFLLYERLKPKEAAEW 180

QY 180 EHFAGQQTFFKILSLHPGQKYLQVRCRKP 210  
 |||  
 Db 181 EHFAGQQTFFKILSLHPGQKYLQVRCRKP 211

RESULT 4  
 A30304  
 A:Accession: A30304  
 A:Molecule type: mRNA  
 A:Residues: 1-616 <EDE>  
 A:Cross-references: GB:J04510; NID:G165669; PIDN:AAA31457.1; PID:G165670  
 R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.  
 Int. J. Biochem. 22, 1089-1095, 1990  
 A:Title: Purification and partial sequence of the rabbit mammary gland prolactin recepto  
 A:Reference number: A60380; MUID:91146782; PMID:2289615  
 A:Accession: A60380  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 41-58, 'X', 60-66, 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX', 167  
 A:Note: the amino end of the mature protein was blocked  
 C:Superfamily: cytokine receptor homology  
 C:Keywords: blocked amino end; glycoprotein; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-616/Product: prolactin receptor 2 #status predicted <MAT>  
 F:36-221/Domain: cytokine receptor homology <CRS>

Query Match 99.1%; Score 1155.5; DB 2; Length 376;  
 Best Local Similarity 99.5%; Pred. No. 5.8e-95;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLLQQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60  
 |||  
 Db 1 MKNVASATVFTLLFLNTCLLQQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60

QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELIVD 119  
 |||  
 Db 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNATQMGSSFSDELIVD 120

QY 120 VTIYVQDPPLLEAVEKQPEDEKPKYLIWKWSPTLIDLTGTFLLYERLKPKEAAEW 179  
 |||  
 Db 121 VTIYVQDPPLLEAVEKQPEDEKPKYLIWKWSPTLIDLTGTFLLYERLKPKEAAEW 180

QY 180 EHFAGQQTFFKILSLHPGQKYLQVRCRKP 210  
 |||  
 Db 181 EHFAGQQTFFKILSLHPGQKYLQVRCRKP 211

F:235-258/Domain: transmembrane #status predicted <TM>  
F:59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 80.2%; Score 935.5; DB 2; Length 616;  
Best Local Similarity 78.7%; Pred. No. 3.5e-75;  
Matches 166; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPFGTDGGLPTNY 60  
Db 1 MKNVASMIVFLLLFLNELLKQSPGPKPFIFKCRSEKETFTCWRRPFGADGGLPTNY 60

QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVD 119  
Db 61 TLTYHKEGETLHECPDYITGGPNSCYFSKHTSIWTIITVNATNQMGSSVSDRYVD 120

QY 120 VTYIVOPDPPELAVKQEDRPKPYLWIKWSPPTLIDLKTGWFTLLYELRLKPEKAAEW 179  
Db 121 VTYIVEPDPNLTLEVKHEDRPKPYLWIKWSPPTLIDLVRSGLTLYELRLKPEKAAEW 180

QY 180 EHFAGQQTQFKILSLHPGQKYLQVRCRKP 210  
Db 181 ETHFAGQQTQFKILSLYPGQKYLQVRCRKP 211

RESULT 5  
I45971  
prolactin receptor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 28-Jul-2000  
C:Accession: I45971  
R:Scott, P.; Kessler, M.A.; Schuler, L.A.  
Mol. Cell. Endocrinol. 89, 47-58, 1992  
A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin  
A:Reference number: I45971; MUID:93246019; PMID:1338725  
A:Accession: I45971  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-581 <SCO>  
A:Cross-references: GB:L02549; NID:g163617; PID:AAA51417.1; PID:g163618  
A:Gene: PRLR  
C:Genetics:  
C:Superfamily: cytokine receptor homology  
F:36-221/Domain: cytokine receptor homology <CRS>

Query Match 74.2%; Score 865.5; DB 2; Length 581;  
Best Local Similarity 70.6%; Pred. No. 5.3e-69;  
Matches 149; Conservative 27; Mismatches 34; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPFGTDGGLPTNY 60  
Db 1 MKNVASRVFILLFLSVLLNGQSPPEKPKLVKCRSPGKETFTCWRRPFGADGGLPTNY 60

QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNA-TOMGSSFSDELYVD 119  
Db 61 TLTYHKEGETLHECPDYITGGPNSCYFSKHTSIWKMYITVNAINQMGISSSDPLYVH 120

QY 120 VTYIVOPDPPELAVKQEDRPKPYLWIKWSPPTLIDLKTGWFTLLYELRLKPEKAAEW 179  
Db 121 VTYIVEPDPNLTLEVKHEDRPKPYLWIKWSPPTMTDVKSGFTIIQYELRLKPEKATDW 180

QY 180 EHFAGQQTQFKILSLHPGQKYLQVRCRKP 210  
Db 181 ETHF"LKQTQLKIFNLYPGQKYLQVRCRKP 211

RESULT 6  
A29884  
prolactin receptor precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 28-Jul-2000  
C:Accession: A29884  
R:Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shiota, M.; Banville  
Cell 53, 69-77, 1988

A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth h  
A:Reference number: A29884; MUID:88165059; PMID:2832068  
A:Accession: A29884  
A:Molecule type: mRNA  
A:Residues: 1-310 <BOU>  
A:Cross-references: GB:M19304; NID:g206364; PIDN:AAA41937.1; PID:g206365  
A:Superfamily: cytokine receptor homology  
C:Keywords: transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-310/Product: prolactin receptor #status predicted <MAT>  
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 71.8%; Score 837; DB 2; Length 310;  
Best Local Similarity 72.7%; Pred. No. 8.6e-64;  
Matches 149; Conservative 20; Mismatches 34; Indels 2; Gaps 2;

QY 7 SATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPFGTDGGLPTNYSLYHR 66  
Db 3 SALAFVLIV-LNISLLKQSPGPKPEIHKCRSPDKETFTCWRRPFGTDGGLPTNYSLYSK 61

QY 67 EGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVDVTVYVQ 125  
Db 62 EGEKTTYECPDYKTSGNPCFQYTSIKYIITVNATNQMGSSSDPLYVDVTVYVE 121

QY 126 PDPLELAVKQEDRPKPYLWIKWSPPTLIDLKTGWFTLLYELRLKPEKAAEWIHFAG 185  
Db 122 PEPPNLTLEVKQLKDKTYLWIKWSPPTITDVKTGWTMEYELRLKPEAEWEIHFAG 181

QY 186 QTEFKILSLHPGQKYLQVRCRKP 210  
Db 182 HQTEKVFDPGQKYLQVRCRKP 206

RESULT 7  
A41070  
prolactin receptor Nb2 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 12-Jun-1992 #sequence\_revision 12-Jun-1992 #text\_change 28-Jul-2000  
C:Accession: A41070; I55417  
R:Ali, S.; Pellsgrini, I.; Kelly, P.A.  
J. Biol. Chem. 266, 20110-20117, 1991  
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of prolac  
A:Reference number: A41070; MUID:92041834; PMID:1718958  
A:Accession: A41070  
A:Molecule type: mRNA  
A:Residues: 1-412 <ALI>  
A:Cross-references: GB:M74152; NID:g206389; PIDN:AAA41946.1; PID:g206390  
R:O'Neal, K.D.; Yu-Dee, L.Y.  
J. Biol. Chem. 269, 26076-26082, 1994  
A:Title: Differential signal transduction of the short, Nb2, and long prolactin recepto  
A:Reference number: I55417; MUID:95014432; PMID:7929319  
A:Accession: I55417  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-412 <RES>  
A:Cross-references: EMBL:U07567; NID:g641963; PIDN:AAA61784.1; PID:g641964  
A:Experimental source: Nb2-11C cell line  
C:Superfamily: cytokine receptor homology  
C:Keywords: transmembrane protein  
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 71.8%; Score 837; DB 2; Length 412;  
Best Local Similarity 72.7%; Pred. No. 1.2e-66;  
Matches 149; Conservative 20; Mismatches 34; Indels 2; Gaps 2;

QY 7 SATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWRRPFGTDGGLPTNYSLYHR 66  
Db 3 SALAFVLIV-LNISLLKQSPGPKPEIHKCRSPDKETFTCWRRPFGTDGGLPTNYSLYSK 61

QY 67 EGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVDVTVYVQ 125  
Db 62 EGEKTTYECPDYKTSGNPCFQYTSIKYIITVNATNQMGSSSDPLYVDVTVYVE 121









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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:11:30 ; Search time 17 Seconds  
(without alignments)  
643.220 Million cell updates/sec

Title: US-10-029-079-3

Perfect score: 1166

Sequence: 1 MKENVASATVFTLLPLNTC.....KILSLHPGQKYLQVRCXP 210

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1155.5	99.1	622	1	PRLR_HUMAN
2	935.5	80.2	616	1	PRLR_RABIT
3	901.5	77.3	581	1	PRLR_CEREL
4	865.5	74.2	581	1	PRLR_BOVIN
5	863.5	74.1	581	1	PRLR_SHEEP
6	837	71.8	610	1	PRLR_RAT
7	813.5	69.8	608	1	PRLR_MOUSE
8	688.5	59.0	831	1	PRLR_CHICK
9	683.5	58.6	830	1	PRLR_COLLI
10	682	58.5	831	1	PRLR_MELGA
11	549.5	47.1	630	1	PRLR_ORENI
12	299	25.6	611	1	GHR_COLLI
13	296	25.4	608	1	GHR_CHICK
14	291.5	25.0	638	1	GHR_RAT
15	280.5	24.9	634	1	GHR_BOVIN
16	280.5	24.9	638	1	GHR_PIG
17	289.5	24.8	638	1	GHR_RABIT
18	278.5	23.9	634	1	GHR_SHEEP
19	277.5	23.8	650	1	GHR_MOUSE
20	262.5	22.5	638	1	GHR_HUMAN
21	259.5	22.3	638	1	GHR_MACMU
22	190.5	16.3	837	1	GCSE_MOUSE
23	165	14.2	918	1	IL6B_HUMAN
24	163	14.0	836	1	GCSR_HUMAN
25	138	11.5	917	1	IL6B_MOUSE
26	134.5	11.5	918	1	IL6B_RAT
27	134	11.4	372	1	CNTR_HUMAN
28	133	11.5	362	1	CNTR_CHICK
29	131	11.2	372	1	CNTR_RAT
30	127	10.9	1165	1	LEPR_PIG
31	126	10.8	380	1	IL32_HUMAN
32	125	10.7	462	1	IL6A_RAT
33	124	10.6	460	1	IL6A_MOUSE

34	120	10.3	1162	1	LEPR_MOUSE
35	116.5	10.0	467	1	IL6A_PIG
36	115	9.9	1451	1	MYM1_HUMAN
37	113.5	9.7	427	1	IL31_HUMAN
38	113.5	9.7	1162	1	LEPR_RAT
39	109.5	9.4	468	1	IL6A_HUMAN
40	109.5	9.4	1165	1	LEPR_HUMAN
41	107	9.2	379	1	CYRG_BOVIN
42	104	8.9	415	1	IL5R_MOUSE
43	103.5	8.9	862	1	IL2S_HUMAN
44	102.5	8.8	507	1	EPOR_MOUSE
45	102.5	8.8	507	1	EPOR_RAT

## ALIGNMENTS

RESULT 1

PRLR\_HUMAN  
ID PRLR\_HUMAN STANDARD; PRT; 622 AA.  
AC P16471; Q9BX87;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1990 (Rel. 15, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Prolactin receptor precursor (PRL-R).  
GN PRLR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=90114212; PubMed=2558309;  
RA Boutin J.-M., Edery M., Shiota M., Jolicoeur C., Lesueur L.,  
Ali S., Gould D., Djiane J., Kelly P.A.;  
RT "Identification of a cDNA encoding a long form of prolactin receptor  
in human hepatoma and breast cancer cells.";  
RL Mol. Endocrinol. 3:1455-1461(1989).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=99182102; PubMed=10084611;  
RA Hu Z.-Z., Zhuang L., Meng J., Leonidres M., Dufau M.L.;  
RT "The human prolactin receptor gene structure and alternative promoter  
utilization: the generic promoter hpIII and a novel human promoter  
hp(N).";  
RL J. Clin. Endocrinol. Metab. 84:1153-1156(1999).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RC TISSUE=Breast carcinoma;  
RA Kline J.B., Clevenger C.V.;  
RT "Characterization of a novel and functional human prolactin receptor  
isoform (delta-S1 PRLr) containing only one extracellular  
fibronectin-like domain.";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.  
RX MEDLINE=95075462; PubMed=7984244;  
RA Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;  
RT "The X-ray structure of a growth hormone-prolactin receptor complex.";  
RL Nature 372:478-481(1994).  
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone prolactin.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=P16471-1; Sequence=Displayed;  
CC Name=2; Synonyms=Delta-S1;  
CC IsoId=P16471-2; Sequence=VSP\_001720;  
CC -!- SIMILARITY: belongs to the type I cytokine family of receptors.  
CC -!- Subfamily 1.  
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.

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EMBL; M31661; AAA60174.1; --  
 EMBL; AF091870; AAD32032.1; --  
 EMBL; AF091863; AAD32032.1; JOINED.  
 EMBL; AF091864; AAD32032.1; JOINED.  
 EMBL; AF091865; AAD32032.1; JOINED.  
 EMBL; AF091866; AAD32032.1; JOINED.  
 EMBL; AF091867; AAD32032.1; JOINED.  
 EMBL; AF091868; AAD32032.1; JOINED.  
 EMBL; AF091869; AAD32032.1; JOINED.  
 EMBL; AF349399; AAK32703.1; --  
 PIR; A40144; A40144.  
 PDB; LBP3; 23-SEP-98.  
 Genew; HGNC:9446; PRLR.  
 MIM; 176761; --  
 GO; GO:0004325; P:prolactin receptor activity; TAS.  
 GO; GO:0007566; P:embryo implantation; TAS.  
 GO; GO:0007595; P:lactation; TAS.  
 InterPro; IPR002996; CR1A.  
 InterPro; IPR008957; FN\_III-like.  
 InterPro; IPR003961; FN\_III.  
 InterPro; IPR003528; Hemtopoptn\_L\_Fl.  
 Pfam; PF00041; fn3; 2.  
 SMART; SM00060; FN3; 2.  
 PROSITE; PS01352; HEMATOPO REC\_L\_Fl; 1.  
 Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 Alternative splicing; 3D-structure.

FT SIGNAL 1 24  
 FT CHAIN 25 622  
 FT DOMAIN 25 234  
 FT TRANSMEM 235 258  
 FT DOMAIN 259 622  
 FT DOMAIN 123 227  
 FT DISULFID 36 46  
 FT CARBOHYD 59 59  
 FT CARBOHYD 104 104  
 FT CARBOHYD 233 233  
 FT VARSPLIC 24 124  
 FT STRAND 31 38  
 FT STRAND 44 50  
 FT STRAND 61 66  
 FT STRAND 73 74  
 FT TURN 80 81  
 FT STRAND 85 88  
 FT TURN 91 92  
 FT STRAND 98 106  
 FT STRAND 112 113  
 FT STRAND 117 120  
 FT HELIX 121 123  
 FT STRAND 125 125  
 FT STRAND 134 134  
 FT STRAND 138 138  
 FT STRAND 146 146  
 FT STRAND 149 150  
 FT TURN 155 156  
 FT TURN 159 162  
 FT STRAND 166 174  
 FT STRAND 181 186  
 FT TURN 187 187  
 FT STRAND 190 191  
 FT TURN 198 199  
 FT STRAND 201 210  
 FT TURN 211 212

FT STRAND 224 225  
 SQ SEQUENCE 622 AA; 69505 MW; DB7FD0328605C787 CRC64;  
 Query Match 99.1%; Score 1155.5; DB 1; Length 622;  
 Best Local Similarity 99.5%; Pred. No. 1.3e-100;  
 Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTQWRPGTGGGLPTNY 60  
 DB 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTQWRPGTGGGLPTNY 60  
 QY 61 SLTVHREGETLMHECPDYITGGPNSCHFGKQYTSMMRTYIMVNAT-QMGSSFSDELYVD 119  
 DB 61 SLTVHREGETLMHECPDYITGGPNSCHFGKQYTSMMRTYIMVNATQMGSSFSDELYVD 120  
 QY 120 VTYIVQDDPPELAVEVQKPEDRKPYLWIKWSPTLLDLATGWFTLLYELRLKPKAAEW 179  
 DB 121 VTYIVQDDPPELAVEVQKPEDRKPYLWIKWSPTLLDLATGWFTLLYELRLKPKAAEW 180  
 QY 180 EIHFGAGQOTEFKILSLHPGQKYLQVRCKPD 210  
 DB 181 EIHFGAGQOTEFKILSLHPGQKYLQVRCKPD 211  
 RESULT 2  
 PRLR\_RABIT  
 ID PRLR\_RABIT STANDARD; PRT; 616 AA.  
 AC P14787;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R).  
 GN PRLR.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=89184578; PubMed=2928321;  
 RA Edery M., Jolicoeur C., Levi-Meyueis C., Dusanter-Fourt I.,  
 RA Petridou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.;  
 RT "Identification and sequence analysis of a second form of prolactin  
 RT receptor by molecular cloning of complementary DNA from rabbit  
 RT mammary gland.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).  
 RN [2]  
 RP 3D-STRUCTURE MODELING OF 30-228.  
 RX MEDLINE=97248733; PubMed=9094747;  
 RA Halaby D., Thoreau E., Djiane J., Mornon J.-P.;  
 RT "Homology modeling of rabbit prolactin hormone complexed with its  
 RT receptor.";  
 RL Proteins 27:459-468(1997).  
 CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone  
 CC prolactin.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily I.  
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
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DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 616
FT DOMAIN 25 234
FT TRANSMEM 235 258
FT DOMAIN 259 616
FT DOMAIN 125 122
FT DOMAIN 124 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 104 104
FT CARBOHYD 132 132
FT CARBOHYD 132 132
FT STRAND 36 38
FT STRAND 44 46
FT STRAND 50 50
FT STRAND 55 55
FT STRAND 61 65
FT STRAND 73 74
FT STRAND 77 77
FT TURN 83 84
FT STRAND 86 88
FT TURN 91 92
FT STRAND 98 104
FT TURN 109 110
FT STRAND 118 120
FT TURN 121 124
FT STRAND 125 125
FT STRAND 131 137
FT STRAND 147 152
FT TURN 160 161
FT STRAND 167 174
FT STRAND 181 182
FT STRAND 186 186
FT STRAND 190 193
FT TURN 198 199
FT STRAND 202 209
FT STRAND 222 223
SQ SEQUENCE 616 AA; 68840 MW; 800E3166FE7108C CRC64;

Query Match 80.2%; Score 935.5; DB 1; Length 616;
Best Local Similarity 78.7%; Pred. No. 5.3e-80;
Matches 166; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
DB 1 MKNVASMTVFLLLFLNRLKQSPGKPFIFKCRSPKEFTTCWRPGADGGLPTNY 60
QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSNWRTYIMMUNA-TQMGSSFSDELYVD 119
DB 61 TLTYHKEGETLHECPDYKTYGPNCTYFSKKHTSIWLYITVNAINQMGSSVSDRYVD 120
QY 120 VTYIVQDDPPELAVEKQEDRPYLIWKSPPTLDLKTGFTLLYEIRLKPEKAAEW 179
DB 121 VTYIVEPDPVNLVLEVKHPEDRPYLIWKSPPTLDVDRSGWLTLOYEIRLKPEKAAEW 180
QY 180 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 210
DB 181 EHFAGQOTQFKILSLYPGQKYLQVVRCKPD 211

RESULT 3
PRLR CEREL STANDARD; PRT; 581 AA.
AC Q28235;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

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DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
OS PRLR.
GN Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
NCBI_TaxID=99860;
RN [1]
RX MEDLINE=96030711; PubMed=7561644;
RA Clarke L.A., Edey M., Loudon A.S., Randall V.A., Postel-Vinay M.C.,
RA Kelly P.A., Jabbour H.N.;
RT "Expression of the prolactin receptor gene during the breeding and
RT non-breeding seasons in red deer (Cervus elaphus): evidence for the
RT expression of two forms in the testis.";
RL J. Endocrinol. 146:313-321(1995).
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone
CC prolactin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X34953; CAA64419.1; -.
CC HSP; P14787; IAN3.
CC InterPro; IPR002996; CRIA.
CC InterPro; IPR008957; FN III-like.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR003528; Hemtopoptn_L_F1.
CC Pfam; PF00041; fn3; 2.
CC SMART; SM00060; FN3; 1.
CC PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 234
FT TRANSMEM 235 258
FT DOMAIN 259 581
FT DOMAIN 25 122
FT DOMAIN 123 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 132 132
FT CARBOHYD 233 233
SQ SEQUENCE 581 AA; 65159 MW; 975E47CB63CF28C CRC64;

Query Match 77.3%; Score 901.5; DB 1; Length 581;
Best Local Similarity 74.4%; Pred. No. 7.7e-77;
Matches 157; Conservative 24; Mismatches 29; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWRRPGTDGGLPTNY 60
DB 1 MKNVASRAVFTLLFLNLTCLLNGQSPGKPKIIFKCRSPGKFTTCWRPGDGLPTNY 60
QY 61 SLTYHREGTLMHECPDYITGGPNSCHFGKQYTSNWRTYIMMUNA-TQMGSSFSDELYVD 119
DB 61 TLTYHKEGETLHECPDYKTYGPNCTYFSKKHTSIWLYITVNAINQMGSSVSDRYVD 120
QY 120 VTYIVQDDPPELAVEKQEDRPYLIWKSPPTLDLKTGFTLLYEIRLKPEKAAEW 179
DB 121 VTYIVEPDPVNLVLEVKHPEDRPYLIWKSPPTLDVDRSGWLTLOYEIRLKPEKAAEW 180

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QY 180 EHFAGQOTFEKILSLHPGQKYLVOVRCKPD 210  
 Db 181 EHFAGQOTFEKILSLHPGQKYLVOVRCKPD 211

RESULT 4

PRLR\_BOVIN STANDARD; PRT: 581 AA.  
 AC Q28172; Q18880; 046591;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R).  
 GN PRLR.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM LONG).  
 RC TISSUE=Endometrium;  
 RX MEDLINE=93246019; PubMed=1338725;  
 RA Scott P., Kessler M.A., Schuler L.A.;  
 RT "Molecular cloning of the bovine prolactin receptor and distribution  
 of prolactin and growth hormone receptor transcripts in fetal and  
 utero-placental tissues.";  
 RL Mol. Cell. Endocrinol. 89:47-58(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM SHORT), AND TISSUE SPECIFICITY.  
 RC TISSUE=Endometrium;  
 RX MEDLINE=97375450; PubMed=9231767;  
 RA Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;  
 RT "Prolactin receptor heterogeneity in bovine fetal and maternal  
 tissues.";  
 RL Endocrinology 138:3187-3194(1997).  
 RN [3]  
 RP SEQUENCE OF 25-234 FROM N.A., AND SEQUENCE OF 25-33.  
 RC TISSUE=Mammary gland;  
 RX MEDLINE=95256770; PubMed=7738463;  
 RA Tchelet A., Staten N.R., Creely D.P., Krivi G.G., Gertler A.;  
 RT "Extracellular domain of prolactin receptor from bovine mammary gland:  
 expression in Escherichia coli, purification and characterization of  
 its interaction with lactogenic hormones.";  
 RL J. Endocrinol. 144:393-403(1995).  
 RN [4]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=98001468; PubMed=9343303;  
 RA Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;  
 RT "Long and short forms of the ovine prolactin receptor: cDNA cloning  
 and genomic analysis reveal that the two forms arise by different  
 alternative splicing mechanisms in ruminants and in rodents.";  
 RL J. Mol. Endocrinol. 19:109-120(1997).  
 CC -1- FUNCTION: This is a receptor for the anterior pituitary hormone  
 prolactin.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Long;  
 CC IsoId=Q28172-1; Sequence=Displayed;  
 CC Name=Short;  
 CC IsoId=Q28172-2; Sequence=VSP\_001718, VSP\_001719;  
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues examined; liver,  
 CC peripheral blood lymphocytes, endometrium, corpus luteum,  
 CC intestine, fetal thymus, fetal spleen, fetal liver and fetal  
 CC brain.  
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
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 CC -----  
 DR EMBL; L02549; AAB51417.1; -;  
 DR EMBL; AF027403; AAB83999.1; -;  
 DR EMBL; AF042780; AAB97748.1; -;  
 DR EMBL; AF042780; AAB97747.1; ALT\_SEQ.  
 DR PIR; I45971; I45971.  
 DR HSP; P14787; IAN3.  
 DR InterPro; IPR002996; CRIA.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR003961; FN\_III.  
 DR Pfam; PF00041; fn3; 2.  
 DR SMART; SM00060; FN3; 2.  
 DR PROSITE; PS01352; HEMATOPO REC L\_F1; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing;  
 FT SIGNAL 1 24 PROBABLE.  
 FT CHAIN 25 581 PROLACTIN RECEPTOR.  
 FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 238 258 POTENTIAL.  
 FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 123 227 FIBRONECTIN TYPE-III 2.  
 FT DISULFID 36 46 BY SIMILARITY.  
 FT DISULFID 75 86 BY SIMILARITY.  
 FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT VARSPLIC 286 296 KKGSEELRAL -> ISQPSRLVSMF (in isoform  
 Short).  
 FT VARSPLIC 297 581 /FTId=VSP\_001718.  
 FT Missing (in isoform Short).  
 FT /FTId=VSP\_001719.  
 FT H -> D (IN REF. 3).  
 FT CONFLICT 120 120 E -> D (IN REF. 3).  
 FT CONFLICT 128 128 L -> V (IN REF. 3).  
 FT CONFLICT 137 137 E -> H (IN REF. 3).  
 FT CONFLICT 141 141 MT -> IM (IN REF. 3).  
 FT CONFLICT 156 157 L -> P (IN REF. 3).  
 FT CONFLICT 186 186  
 SQ SEQUENCE 581 AA; 65153 MW; 7385C0D6956EE139 CRC64;  
 Query Match 74.2%; Score 865.5; DB 1; Length 581;  
 Best Local Similarity 70.6%; Pred. No. 1.8e-73;  
 Matches 149; Conservative 27; Mismatches 34; Indels 1; Gaps 1;  
 QY 1 MKNVASATVFTLLFLNLTCLNGQLPPGAPETFKCRSPNKETFTCWWRPGTGGGLPTNY 60  
 Db 1 MKNASRVVFILLFLSVSLNGQSPPEKPKLVKCRSPGKETFTCWWRPGTGGGLPTNY 60  
 QY 61 SLTVHREGETLMEHCDDYITGGNSCHFGKQYTMRTYIMVNA-TQMGSSPSFDELYVD 119  
 Db 61 TLTVHKEGTELMEHCDDYITGGNSCHFGKQYTMRTYIMVNA-TQMGSSPSFDELYVD 120  
 QY 120 VTIIVQDPPLEAVEVQKQEDRPKYLWIKWSPTTIDKTGWTLLYIRLKPXAAEW 179  
 Db 121 VTIVEPEPPANLTLELKHEDRPKYLWIKWSPTTIDKTGWTLLYIRLKPXATDW 180  
 QY 180 EHFAGQOTFEKILSLHPGQKYLVOVRCKPD 210  
 Db 181 EHFAGQOTFEKILSLHPGQKYLVOVRCKPD 211

RESULT 5

PRLR\_SHEEP STANDARD; PRT: 581 AA.  
 AC Q4553; Q46569; 046573; 046574; P79203; P79205;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R) (OPR).



RC STRAIN=Sprague-Dawley; TISSUE=Ovary;  
 RX MEDLINE=90241201; PubMed=2159291;  
 RA Zhang R., Buczko E., Tsai-Morris C.-H., Hu Z.-Z., Dufau M.L.;  
 RT "Isolation and characterization of two novel rat ovarian lactogen  
 RL receptor cDNA species.";  
 RL Biochem. Biophys. Res. Commun. 168:415-422(1990).  
 RN [3]  
 RP SEQUENCE OF 281-610 FROM N.A.  
 RA Banville D., Stocco R., Murthy K.K., Boie Y., Kelly P.A.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=80165059; PubMed=2832068;  
 RA Boutin J.-M., Jolicoeur C., Okamura H., Gagnon J., Edery M.,  
 RA Shirota M., Banville D., Dusanter-Fourt I., Djiane J., Kelly P.A.;  
 RT "Cloning and expression of the rat prolactin receptor, a member of  
 RL the growth hormone/prolactin receptor gene family.";  
 RN Cell 53:69-77(1988).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RC TISSUE=Lymphoma;  
 RX MEDLINE=92041834; PubMed=1718958;  
 RA Ali S., Pelligrini I., Kelly P.A.;  
 RT "A prolactin-dependent immune cell line (Nb2) expresses a mutant form  
 RL of prolactin receptor.";  
 RN J. Biol. Chem. 266:20110-20117(1991).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RX MEDLINE=95014432; PubMed=7929319;  
 RA O'Neal K.D., Yu-Lee L.Y.;  
 RT "Differential signal transduction of the short, Nb2, and long  
 RL prolactin receptors. Activation of interferon regulatory factor-1 and  
 RT cell proliferation.";  
 RN J. Biol. Chem. 269:26076-26082(1994).  
 CC -1- FUNCTION: This is a receptor for the anterior pituitary hormone  
 prolactin.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=Long;  
 CC IsoId=P05710-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Short;  
 CC IsoId=P05710-2; Sequence=VSP\_001725, VSP\_001726;  
 CC Name=3; Synonyms=Medium;  
 CC IsoId=P05710-3; Sequence=VSP\_001727, VSP\_001728;  
 CC Name=4; Synonyms=Nb2;  
 CC IsoId=P05710-4; Sequence=VSP\_001729;  
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M57668; AAA41938.1; -  
 CC EMBL; M34083; AAA79273.1; -  
 CC EMBL; L48060; AAA79274.1; -  
 CC EMBL; U34730; AAA32053.1; -  
 CC EMBL; M19304; AAA41937.1; -  
 CC EMBL; M74152; AAA41946.1; -  
 CC EMBL; U07567; AAA61784.1; -  
 CC PIR; A29884; A29884.  
 CC PIR; A34631; A34631.  
 CC PIR; A36116; A36116.  
 CC PIR; A41070; A41070.  
 CC PIR; B34631; B34631.  
 CC PDB; 1F6F; 20-DEC-00.

DR InterPro; IPR002996; CRIA.  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR003961; FN-III.  
 DR InterPro; IPR003288; Hemopoetn\_L\_F1.  
 DR Pfam; PF00041; fn3; 2.  
 DR SMART; SM00060; FN3; 2.  
 DR PROSITE; PS01352; HEMATOPO REC L\_F1; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing; 3D-structure.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 610 PROLACTIN RECEPTOR.  
 FT DOMAIN 20 229 EXTRACELLULAR (BY SIMILARITY).  
 FT TRANSMEM 230 253 BY SIMILARITY.  
 FT DOMAIN 254 610 CYTOPLASMIC (BY SIMILARITY).  
 FT DOMAIN 20 117 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 119 222 FIBRONECTIN TYPE-III 2.  
 FT DISULFID 31 41 BY SIMILARITY.  
 FT DISULFID 70 81 BY SIMILARITY.  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPLIC 131 150 EVKQKDKKTYLWVKSPPT -> DYRWEVSHQCHQALPKSA  
 FT VARSPLIC 151 610 KLN (in isoform 2).  
 FT VARSPLIC 281 310 Missing (in isoform 2).  
 FT VARSPLIC 311 610 Missing (in isoform 3).  
 FT VARSPLIC 342 539 Missing (in isoform 4).  
 FT CONFLICT 236 236 V -> A (IN REF. 2).  
 FT CONFLICT 345 345 G -> V (IN REF. 2).  
 FT CONFLICT 465 465 E -> K (IN REF. 1).  
 FT CONFLICT 466 466 Q -> E (IN REF. 2).  
 FT CONFLICT 469 469 A -> G (IN REF. 2).  
 FT CONFLICT 541 541 T -> M (IN REF. 1).  
 FT CONFLICT 555 555 Q -> K (IN REF. 2).  
 SQ SEQUENCE 610 AA; 68599 MW; 83D04D832861295D CRC64;  
 Query Match 71.8%; Score 837; DB 1; Length 610;  
 Best Local Similarity 72.7%; Pred. No. 9e-71;  
 Matches 149; Conservative 20; Mismatches 34; Indels 2; Gaps 2;  
 QY 7 SATVFTLLFLINTCLNGQLPPGKPEIFKCRSPKXETFTTCWPRPGTDGGLPTNYSLYHR 66  
 DB 3 SALAFVLLV-LNISLLKGQSPGKPEIHKCRSPDKETFTCWNPNGTDGGLPTNYSLYTSK 61  
 QY 67 EGETLMECEPDYITGGPNSCHFGKQYTSWRTYIMVNAT-OMGSSFSDELYVDVTVYQ 125  
 DB 62 EGETTYECDYKTSGNPSCFFSKQYTSIWKIYITVNATNQMGSSSDPLYVDVTVIVE 121  
 QY 126 PDPLELAEVQKPEDRPYLMWIKWSPPTLIDLTGNTFTLLYRILKPKAAEWEIHFAG 185  
 DB 122 PEPRNLTLVEKQLDKKTYLWVKWSPPTTIDVKTGTFMEYRILKPEAEWEIHFAG 181  
 QY 186 QQTEFKLSLHFGKQYLVQVCKPD 210  
 DB 182 HQIQKRVFDLYPGQKYLVTQCKPD 206  
 RESULT 7  
 PRLR MOUSE  
 ID PRLR MOUSE STANDARD; PRT; 508 AA.  
 AC Q08501; P15212; P15213; Q62099;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R).  
 GN PRLR.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM PRL-R3).  
 RC STRAIN=C3H; Tissue=Mammary Gland;  
 RX MEDLINE=94085789; PubMed=8262385;  
 RA Moore R.C., Oka T.;  
 RT "Cloning and sequencing of the cDNA encoding the murine mammary gland  
 RL long-form prolactin receptor.";  
 RL Gene 134:263-265(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM PRL-R3).  
 RC STRAIN=Swiss Webster; Tissue=Liver;  
 RX MEDLINE=93307149; PubMed=8319571;  
 RA Clarke D.L., Linzer D.I.H.;  
 RT "Changes in prolactin receptor expression during pregnancy in the  
 RL mouse ovary.";  
 RL Endocrinology 133:224-232(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM PRL-R3).  
 RA Sasaki M.;  
 RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM PRL-R3).  
 RC STRAIN=BALB/c; Tissue=Mammary Gland;  
 RA Edery M., Peret A., Nandi S., Kelly P.A.;  
 RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORMS PRL-R2 AND PRL-R1).  
 RC STRAIN=Swiss Webster; Tissue=Liver;  
 RX MEDLINE=89261824; PubMed=2725531;  
 RA Davis J.A., Linzer D.I.H.;  
 RT "Expression of multiple forms of the prolactin receptor in mouse  
 RL liver.";  
 RL Mol. Endocrinol. 3:674-680(1989).  
 CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone  
 CC prolactin.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=PRL-R3; Sequence=Displayed;  
 CC IsoId=Q08501-1; Sequence=VSP\_001723, VSP\_001724;  
 CC Name=PRL-R1;  
 CC IsoId=Q08501-2; Sequence=VSP\_001723, VSP\_001722;  
 CC Name=PRL-R2;  
 CC IsoId=Q08501-3; Sequence=VSP\_001721, VSP\_001722;  
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -----  
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 CC -----  
 CC EMBL; L13593; AAC37641.1; -  
 CC EMBL; L14811; AAA02686.1; -  
 CC EMBL; D10214; BAA01066.1; -  
 CC EMBL; X73372; CAA51789.1; -  
 CC EMBL; M22959; AAA39977.1; -  
 CC EMBL; M22958; AAA39976.1; -  
 CC PIR; I53269; I53269.  
 CC PIR; I7524; I7524.  
 CC PIR; I7525; I7525.  
 CC HSP; P16471; I1B3.  
 CC MGD; MGI:97763; ERL.  
 CC InterPro; IPR002996; CRIA.  
 CC InterPro; IPR008957; FN\_III-like.  
 CC InterPro; IPR003961; FN\_III.

DR InterPro: IPR003528; Hemtopoptn\_L\_F1.  
 DR Pfam: PF00041; FN3; 2.  
 DR SMART: SMO0060; FN3; 2.  
 DR PROSITE: PS01352; HEMATOPOI\_REC\_L\_F1; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;  
 KW Alternative splicing.  
 FT SIGNAL 1 19  
 FT CHAIN 20 608  
 FT DOMAIN 20 229  
 FT BY SIMILARITY.  
 FT TRANSMEM 230 253  
 FT DOMAIN 254 608  
 FT DOMAIN 20 117  
 FT DOMAIN 119 222  
 FT BY SIMILARITY.  
 FT DISULFID 31 41  
 FT CYS 70 81  
 FT CARBOHYD 54 54  
 FT CARBOHYD 99 99  
 FT CARBOHYD 127 127  
 FT VARSPLIC 281 292  
 FT  
 FT VARSPLIC 293 608  
 FT  
 FT VARSPLIC 281 303  
 FT  
 FT VARSPLIC 304 608  
 FT  
 FT CONFLICT 558 558  
 FT L -> F (IN REF. 2).  
 FT  
 FT SEQUENCE 608 AA; 68240 MW; B8CE202B2EFC9FC6 CRC64;  
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 Query Match 69.8%; Score 813.5; DB 1; Length 608;  
 Best Local Similarity 69.8%; Pred. No. 1.4e-68;  
 Matches 143; Conservative 25; Mismatches 36; Indels 1; Gaps 1;  
 QY 7 SATVFTLLFLNTCLLNGQLPQPKPEIKCRSPKNETTCWVRPGTGGPLTNYSLTYHR 66  
 DB 2 SSALAYMLLVLSILLNGSPGPKPEIKCRSPDKETTCWVRPGTGGPLTNYSLTYSK 61  
 QY 67 EGETLMHECPDYITGPNNSCHFGKYOTSMWRTYIMVNAT-OMGSSFDELYVDVYIVQ 125  
 DB 62 EGEKNTYECPDYKTSQNSCFESKYOTSIWKIYITVNATNEMSGSTSDPLVDVYIYE 121  
 QY 126 PDPLELAVEVQKPEDRKYPLWKVSPPTLIDLTGWFTLLYELRLKPEKAAEWIHFAG 185  
 DB 122 PEPPRLTLEVKQLDKKTYLWVKLWLPPTITDVKIWNFTMEYELRKSEADEWIIHFTG 181  
 QY 186 QQTEFKILSLHFGQKYLQVQRCKPD 210  
 DB 182 HQTFKVPDLYPGQKYLQVQRCKPD 206  
 RESULT 8  
 PRLR\_CHICK  
 ID\_PRLR\_CHICK STANDARD; PRT; 831 AA.  
 AC Q04594;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R) (CPRLP).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=White Leghorn; Tissue=Kidney;  
 RX MEDLINE=93075121; PubMed=1445292;  
 RA Tanaka M., Maeda K., Okubo T., Nakashima K.;  
 RT "Double antenna structure of chicken prolactin receptor deduced from  
 RT the cDNA sequence.";



RL Biochem. Biophys. Res. Commun. 188:490-496(1992).  
 CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone  
 CC prolactin.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC  
 CC -!- SUBFAMILY: 1.  
 CC  
 CC -!- SIMILARITY: Contains 4 fibronectin type III domains.  
 CC  
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 CC  
 CC EMBL; D13154; BAA02439.1; ..  
 CC PIR; JQ1655; JQ1655.  
 CC HSSP; P16471; 1BP3.  
 CC InterPro; IPR002996; CR1A.  
 CC InterPro; IPR008957; FN\_III-like.  
 CC InterPro; IPR003961; FN\_III.  
 CC Pfam; PF00041; fn3; 4.  
 CC SMART; SM00060; FN3; 4.  
 CC PROSITE; PS01352; HEMATOPO REC L\_F1; 1.  
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 CC SIGNAL 23  
 CC CHAIN 1 23  
 CC DOMAIN 24 831  
 CC TRANSMEM 24 438  
 CC DOMAIN 439 459  
 CC DOMAIN 460 831  
 CC DOMAIN 25 122  
 CC DOMAIN 123 225  
 CC DOMAIN 228 325  
 CC DOMAIN 326 428  
 CC DOMAIN 36 46  
 CC DISULFID 75 86  
 CC CARBOHYD 59 59  
 CC CARBOHYD 91 91  
 CC CARBOHYD 100 100  
 CC CARBOHYD 112 112  
 CC CARBOHYD 132 132  
 CC CARBOHYD 262 262  
 CC CARBOHYD 303 303  
 CC CARBOHYD 315 315  
 CC CARBOHYD 335 335  
 CC SEQUENCE 831 AA; 94102 MW; 1C4E75791DCADBE9 CRC64;  
 SQ  
 Query Match 59.0%; Score 688.5; DB 1; Length 831;  
 Best Local Similarity 61.9%; Pred. No. 1.1e-56;  
 Matches 117; Conservative 32; Mismatches 39; Indels 1; Gaps 1;  
 QY 23 NGOLPFGKPEIKCRSPNKETFTCWRRPGTDCGLPTNYSLTVHREGTLMHCEPDYITGG 82  
 Db 226 SGOSSPEKPTIKCRSPEKETFTCWKPGDGHPTNYLLYSKGESEQVVECPDYRTAG 285  
 QY 83 PMSCHFGKQYTSWRTYIMMVAAT-OMGSSFSDELVDVYTVIQDPDPLEAVEVKQPED 141  
 Db 286 PMSCYFDKHTSPWITNYITVATNMGNSDSDPHVDVYTVIQDPDPPVNTLELKKPIN 345  
 QY 142 RPYLWIKSPPTLDLTKGNTLLYELRLKPEKAAEHIHPAGQOTFKLSLHPGQKY 201  
 Db 346 RPYLVLTWSPPLADVRSGWLTLEYELKPEEGEEMETIFVGQOTQYKMFSLNPGKY 405  
 QY 202 LVQVRCKPD 210  
 Db 406 IQIHKCPD 414  
 RESULT 9  
 PRLR\_COLLI STANDARD; PRT; 830 AA.  
 ID PRLR\_COLLI

AC Q90374;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R).  
 GN PRLR.  
 OS Columba livia (Domestic pigeon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.  
 OX NCBI\_TaxID=8932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cropsac;  
 RX MEDLINE=94283267; PubMed=7516866;  
 RA Chen X., Horseman N.D.;  
 RT "Cloning, expression, and mutational analysis of the pigeon prolactin  
 RL receptor.";  
 RL Endocrinology 135:269-276(1994).  
 CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone  
 CC prolactin.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -!- SIMILARITY: Contains 4 fibronectin type III domains.  
 CC  
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 CC  
 CC EMBL; U07694; AAA20646.1; ..  
 CC PIR; I50455; I50455.  
 CC HSSP; P16471; 1BP3.  
 CC InterPro; IPR002996; CR1A.  
 CC InterPro; IPR008957; FN\_III-like.  
 CC InterPro; IPR003961; FN\_III.  
 CC Pfam; PF00041; fn3; 4.  
 CC SMART; SM00060; FN3; 4.  
 CC PROSITE; PS01352; HEMATOPO REC L\_F1; 1.  
 CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 CC SIGNAL 1 23  
 CC CHAIN 1 23  
 CC DOMAIN 24 830  
 CC TRANSMEM 24 439  
 CC DOMAIN 440 460  
 CC DOMAIN 461 830  
 CC DOMAIN 25 122  
 CC DOMAIN 123 226  
 CC DOMAIN 229 326  
 CC DOMAIN 327 429  
 CC DOMAIN 36 46  
 CC DISULFID 75 86  
 CC CARBOHYD 59 59  
 CC CARBOHYD 91 91  
 CC CARBOHYD 100 100  
 CC CARBOHYD 112 112  
 CC CARBOHYD 132 132  
 CC CARBOHYD 263 263  
 CC CARBOHYD 304 304  
 CC CARBOHYD 316 316  
 CC CARBOHYD 336 336  
 CC SEQUENCE 830 AA; 94507 MW; 3B074E83CDF69EFF CRC64;  
 SQ  
 Query Match 58.6%; Score 683.5; DB 1; Length 830;  
 Best Local Similarity 61.9%; Pred. No. 3.1e-56;  
 Matches 117; Conservative 32; Mismatches 39; Indels 1; Gaps 1;  
 QY 23 NGOLPFGKPEIKCRSPNKETFTCWRRPGTDCGLPTNYSLTVHREGTLMHCEPDYITGG 82  
 Db 227 NGESPEKPTIKCRSPEKETFTCWKPGDGHPTNYLLYSKGESEVVECPDYRTAG 286



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QY 83 PNCSEFGKQYTSWRTYIMMNNAT-OMGSSFSDELVDVYIVQPPPELEAVEKQPED 141
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 287 PNCYDKKHTSWYINIVKATNEIGNSVSDPLVYIVQTDPPVNVITLKKTVN 346
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 142 RKPYLWKNSPPPLIDLKGTWFTLLYIRLKPKEAEWEIHPAGQOTEFKILSLHPGQXY 201
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 347 RKPYLVLTWSPPLADVRSGMLTLDYELRLKPEAEWEIHFVGGQOQTHYKMFSLNPGKXY 406
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 202 LVGVCKPD 210
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 407 IVQIHCKPD 415
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
PRLR_MELGA STANDARD; PRT; 831 AA.
AC Q1094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (TPRLR).
GN PRLR.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagrids.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97057891; PubMed=8902221;
RA Zhou J.F., Zadowny D., Guemene D., Kuhnlein U.;
RT "Molecular cloning, tissue distribution, and expression of the
RT prolactin receptor during various reproductive states in Meleagris
RT gallopavo.";
RL Biol. Reprod. 55:1081-1090(1996).
RN [2]
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RC TISSUE=Ovary;
RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
RA Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DE -!- FUNCTION: This is a receptor for the anterior pituitary hormone
DE prolactin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 4 fibronectin type III domains.
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CC -----
CC EMBL; L76587; AAB01544.1; -.
CC DR EMBL; U22947; AAB75038.1; -.
CC DR EMBL; U22924; AAB75039.1; -.
CC DR HSPF; F16471; IEP3.
CC DR InterPro; IPR002996; CRI1A.
CC DR InterPro; IPR008957; FN III-like.
CC DR InterPro; IPR003961; FN III.
CC DR InterPro; IPR003528; Hemtopoptn_L_F1.
CC DR Pfam; PF00041; fn3; 4.
CC DR SMART; SM00060; FN3; 3.
CC DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 831 PROLACTIN RECEPTOR.
FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 439 459 POTENTIAL.
FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).

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FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.
FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.
FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 831 AA; 94394 MW; 220916320F77FACI CRC64;

Query Match 58.5%; Score 682; DB 1; Length 831;
Best Local Similarity 62.0%; Pred. No. 4.3e-56;
Matches 119; Conservative 31; Mismatches 40; Indels 2; Gaps 2;

QY 21 LINGQL-PPGKPEIFKCSFNKETFTCWVRGDTGGGLPTNYSLYHREGETLMHECPDYI 79
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 223 LTSGLSPPKPTITKCSPEKFTTCWKPLDGGHPTNYTLTYSKRGEEQVTECPDYR 282
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 80 TGGPNSCHFQKQYTSWRTYIMMNNAT-OMGSSFSDELVDVYIVQPPPELEAVEKQ 138
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 283 TAGPNSCYFDKHTSWYINIVKATNEIGNSVSDPLVYIVQTDPPVNVITLKK 342
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 139 PEDRKPYLWKNSPPPLIDLKGTWFTLLYIRLKPKEAEWEIHPAGQOTEFKILSLHPG 198
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 343 PINRKPYLMTWSPPLADVRSGMLTLDYELRLKPEAEWEIHFVGGQOQTHYKMFSLNPG 402
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 199 QKYLQVCKPD 210
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 403 KKYIVQIHCKPD 414
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
PRLR_ORENI STANDARD; PRT; 630 AA.
AC Q91513;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95320210; PubMed=7597076;
RA Sandra O., Sohn F., de Luze A., Prunet P., Edery M., Kelly P.A.;
RA "Expression cloning of a cDNA encoding a fish prolactin receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:6037-6041(1995).
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone
CC prolactin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----

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CC -----
DR EMBL; L34783; AAA98997.1; -.
DR PIR; I51086; I51086.
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 630
FT DOMAIN 24 234
FT TRANSMEM 235 258
FT DOMAIN 259 630
FT DOMAIN 124 123
FT DOMAIN 124 228
FT DISULFID 37 47
FT DISULFID 76 87
FT CARBOHYD 92 92
FT CARBOHYD 101 101
SQ SEQUENCE 630 AA; 70810 MW; A451563F3D12979D CRC64;

Query Match 47.1%; Score 549.5; DB 1; Length 630;
Best Local Similarity 54.6%; Pred. No. 8.1e-44;
Matches 101; Conservative 26; Mismatches 55; Indels 3; Gaps 3;

Qy 28 PGKPEIKFCKSPKKEHTCWRTGGLTNTVSLYTHREGETLMEHCDDYITGGNSCH 87
Db 29 PGKPEIKFCKSPKKEHTCWRTGGLTNTVSLYTHREGETLMEHCDDYITGGNSCH 88
Qy 88 FGQYTSMTWRTYIMVNATQ-MGSSPSDELYVDVTIVOPDPLELAVEVKQPEDRKPYL 146
Db 89 FNKNNTLIWYSYNTVATVATKVTSDPDIDVIVVGHPEKKEVTKM-DQGWPL 147
Qy 147 WIKWSPTLIDLTGWTLLYELRLKPE-KAAWEIHFAGQQTFFKILSLHPGQKYLVOV 205
Db 148 RVSWEPKRAKTRSGMTITLYELRLKPELEDESEWHAAGQQQWFIISLSSGTVLIQV 207
Qy 206 RCKPD 210
Db 208 RCKPD 212

RESULT 12
GHR_COLLI STANDARD; PRT; 611 AA.
AC Q30375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).
DE protein).
DE GHR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cheng C.H.K., Shaw P.C., Tsim K.W.K., Lau K.P.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: This is a receptor for pituitary gland growth hormone.
CC -!- FUNCTION: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -!- SUBFAMILY 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -----

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CC -----
DR EMBL; U20353; AAA84745.1; -.
DR HSSP; P10912; IAXI.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 611
FT DOMAIN 21 240
FT TRANSMEM 241 264
FT DOMAIN 265 611
FT DOMAIN 119 226
FT DISULFID 34 44
FT DISULFID 75 86
FT DISULFID 100 114
FT CARBOHYD 16 16
FT CARBOHYD 53 53
FT CARBOHYD 89 89
FT CARBOHYD 130 130
FT CARBOHYD 135 135
FT CARBOHYD 174 174
SQ SEQUENCE 611 AA; 68851 MW; C48750B9E4EBDA CRC64;

Query Match 25.6%; Score 299; DB 1; Length 611;
Best Local Similarity 34.4%; Pred. No. 2.3e-20;
Matches 72; Conservative 28; Mismatches 89; Indels 20; Gaps 6;

Qy 13 LLLFLNTCLNGQLPPCK-----PEIFKCPSPKKEHTCWRTGGLTNTVSLY 62
Db 6 LLLTLVLVCANDLSASDDVLRLPQISKCKSPLETFSCYW---TDGNFNLAPGTIQL 62
Qy 63 TYHREGETLMEHCDDYITGGNSCHFGQYTSMTWRTY-IMVNATQMGSSPSDELYVDVT 121
Db 63 LYMKRNDKWKCPDYITAGENSCTYNTSYTSIWIPYCVKLVNKDEV---PDEKCFSDV 118
Qy 122 YIVOPDPLELAVEVKQPEDRKPY--LWIKWSPTLIDLTGWTLLYELRLKPEKAAEW 179
Db 119 EIVLPDPPVHLNWTLLNTSGTHGDIQVRWDPPPTADVQKGMWITLEYELQYKEVNETKW 178
Qy 180 EIHFGAQQTFFKILSLHPGQKYLVOVRCK 208
Db 179 KELEPRLSTWVPLVSLKIGRDYEVRSR 207

RESULT 13
GHR_CHICK STANDARD; PRT; 608 AA.
AC Q02092;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).
DE GHR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Liver;
RA MEDLINE=91243665; PubMed=2036984;
RR Burridge J., Liu S.S., Cogburn L.A.;
RT "Molecular cloning of the chicken growth hormone receptor
RT complementary deoxyribonucleic acid: mutation of the gene in
RT sex-linked dwarf chickens.";
RL Endocrinology 138:3183-3192(1991).
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Broad specificity.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -----
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CC -----
CC EMBL; M74057; AAA48781.1; -.
CC PIR; S32823; S32823.
CC DR HSP; P10912; LXI.
CC DR InterPro; IPR002996; CRI1.
CC DR InterPro; IPR008957; FN_III-like.
CC DR InterPro; IPR003961; FN_III.
CC DR InterPro; IPR003528; Hemtopoptn_L_Fl.
CC DR Pfam; PF00041; fn3; 1.
CC DR SMART; SM00060; FN3; 1.
CC DR PROSITE; PS01352; HEMATOPO REC L Fl; 1.
CC KW Receptor; Transmembrane; Glycoprotein; Signal.
CC FT SIGNAL 1 16
CC FT CHAIN 17 608
CC FT DOMAIN 17 237
CC FT TRANSMEM 238 261
CC FT DOMAIN 262 608
CC FT DOMAIN 117 223
CC FT DISULFID 34 44
CC FT DISULFID 72 83
CC FT DISULFID 97 111
CC FT CARBOHYD 86 86
CC FT CARBOHYD 127 127
CC FT CARBOHYD 132 132
CC FT CARBOHYD 171 171
CC SEQUENCE 608 AA; 68572 MW; D71AD7B5C62528DC CRC64;
CC -----
Query Match 25.4%; Score 296; DB 1; Length 608;
Best Local similarity 35.5%; Pred. No. 4.4e-20;
Matches 65; Conservative 30; Mismatches 76; Indels 12; Gaps 5;

QY 31 PFIFKCRSPENKFTFCWWRPGTGGGLPTN--YSLTYHREGETLMHCEPDIYITGGPNSCHF 88
DB 29 PQISKCRSPLETFPCYK--TDGKVITSGTIQLLYMKRSDDEWKCPDIYITAGENSCHF 85
QY 89 GKQYTSMTQTY-IMMVNATQNGSSFSDELYVDVYIVQPPDPLEAVEVKQEDKPY-- 145
DB 86 NTSVTSIMTPYCVKLANDEV----FDEKCFSDVEIPLPDPVHLNKLNTLSQTGIGHD 141
QY 146 LMKWSPPTLIDKYGWFTLVEIRLPEKAAEWHIFAGQQTFFKILSLHPGKYLQV 205
DB 142 IQRWDDPPPTADVQKGWITLSEYELQYKENVETKWKLEPLSLIVPFLYSLKWGRDYEV 201
QY 206 RCK 208
DB 202 RSR 204

RESULT 14
GHR_RAT STANDARD; PRT 638 AA.
ID - GHR RAT

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Db 109 ANSCFFNSYSIWTPYCIKUTT---NGDLDEXCFVTDEIVQDPDPPIGLNWTLLNISLP 165
QY 140 EDRFYLWIKWSPPTLIDKTGWFTLLYEIRLKEPEKAAEWEIHFAGQOTEFKILSLHPGQ 199
Db 166 GIRGD-IQVWQPPSADVLKGMWILEVEIQYKEVNETKWTMTSPIMSTVPLYSRLDK 224
QY 200 KYLVQVRCK 208
Db 225 EHEVRVRSR 233

RESULT 15
GHR_BOVIN
ID_GHR_BOVIN STANDARD; PRT; 634 AA.
AC P7S108;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
GN GHR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GR; TISSUE=Liver;
RA Souza S.C., Wang X., Lobo R.B., Knoch J.J.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X70041; CAA49635.1; --
CC HSSP; P10912; 1A22.
CC InterPro; IPR002996; CR1A.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003528; Hemtopoptn_L_F1.
CC Pfam; PF00041; fn3; 1.
CC SMART; SM00060; FN3; 1.
CC PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1
CC CHAIN 18
CC DOMAIN 19 634 GROWTH HORMONE RECEPTOR.
CC DOMAIN 19 260 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 261 284 POTENTIAL.
CC DOMAIN 285 634 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 141 248 FIBRONECTIN TYPE-III.
CC DISULFID 56 66 BY SIMILARITY.
CC DISULFID 97 108 BY SIMILARITY.
CC DISULFID 122 136 BY SIMILARITY.
CC CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 634 AA; 70979 MW; 91955A28296CBD2E CRC64;

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Query Match 24.9%; Score 290.5; DB 1; Length 634;
Best Local Similarity 34.6%; Pred. No. 1.5e-19;
Matches 64; Conservative 26; Mismatches 86; Indels 9; Gaps 4;

QY 29 GKPEIFKCRSPNKETFTCWWRPGTDGGL--PTNYSLTYYHREGETLMHCEPDYITGGPNSC 86
Db 49 GNPKFTKCRSPELETFSCHWTDGANHSLQSPGVQMFYIRRDIGEWKECPDYVSAGENSC 108
QY 87 HFGKOYTSNWRTYIMVAVNATQWGSFSDLYVDVTYIVQDPDPLEL---AVEVKQPEDRK 143
Db 109 YFNSSYTSVWTPYCIKITS---NGDIVDHKCFSDIVQDPDPVGLNWTLLNISLTHA 165
QY 144 PYLWIKWSPPTLIDKTGWFTLLYEIRLKEPEKAAEWEIHFAGQOTEFKILSLHPGQKYL 203
Db 166 DIL-VKWEPPPTNDVKGWIILEYELHYKELNETQWQMDPLMVTSPMYSRLDKVEYV 224
QY 204 QVRCK 208
Db 225 RVRTR 229

```

Search completed: May 12, 2004, 16:17:57  
Job time : 18 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 12, 2004, 16:14:46 ; Search time 45 Seconds  
(without alignments)  
1472.418 Million cell updates/sec

Title: US-10-029-079-3  
Perfect score: 1166  
Sequence: 1 MKNVASATVFTLLFLNTC.....KILSLHPCQKYLQVRCKPD 210

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1155.5	99.1	268	4 Q8TD78	Q8td78 homo sapien
2	1155.5	99.1	288	4 Q96P36	Q96p36 homo sapien
3	1155.5	99.1	349	4 Q9UHJ5	Q9uhj5 homo sapien
4	1155.5	99.1	376	4 Q96P35	Q96p35 homo sapien
5	1088.5	93.4	622	6 Q85V4	Q85v4 cebus apell
6	1052.5	90.3	622	6 Q9N0J7	Q9noj7 callithrix
7	1036.5	88.9	206	4 Q16354	Q16354 homo sapien
8	888.5	76.2	625	6 Q9XS92	Q9xs92 trichosurus
9	814.5	69.9	292	11 Q8C7G1	Q8c7g1 mus musculus
10	811.5	69.6	608	11 Q99J21	Q99j21 mus musculus
11	764.5	65.6	198	6 Q18985	Q18985 cervus elap
12	759.5	65.1	197	4 Q8TD76	Q8td76 homo sapien
13	759.5	65.1	217	4 Q8TD75	Q8td75 homo sapien
14	758.5	65.1	227	6 Q9GLW3	Q9glw3 ursus marit
15	691.5	59.3	460	13 Q7T220	Q7t220 gallus gall
16	683.5	58.6	217	6 O46386	O46386 mustela vis

#### ALIGNMENTS

RESULT 1

Q8TD78

ID Q8TD78 PRELIMINARY; PRT; 268 AA.

AC Q8TD78; 01-JUN-2002 (TREMblrel. 21, Created)

DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)

DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)

DE Prolactin receptor delta 7/11.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

CX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Breast tumor;

RA Trott J.F., Hovey R.C., Koduri S., Vanderhaar B.K.;

RT "Expression of multiple human prolactin receptor variants in breast

RT and colon cancer derived by splicing to exon 11."

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF492470; AAM18048.1; -

DR GO; GO:0016020; C:membrane; IEA

DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . . ; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR002996; CR1A.

DR InterPro; IPR003961; FN\_III.

DR InterPro; IPR008957; FN\_III-like.

DR InterPro; IPR003528; Hemtopoptn\_L\_F1.

DR Pfam; PF00041; fn3; 2

DR SMART; SM00060; FN3; 2

DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.

SW SEQUENCE 268 AA; 30705 MW; FBB498AB649A078C CRC64;

Query Match 99.1%; Score 1155.5; DB 4; Length 268;

Best Local Similarity 99.5%; Pred. No. 6.6e-109;

Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSNKKTFTCWPGTGGGLPTNY 60

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Db 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNNAT-OMGSSFSDELYVD 119
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNNATQMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKEKAAEW 179
Db 121 VTYIVQDPDPLEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKEKAAEW 180
QY 180 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 210
Db 181 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 2
Q96P36
ID Q96P36 PRELIMINARY; PRT; 288 AA.
AC Q96P36;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DE Prolactin receptor short isoform A.
GN PRLR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20054419; PubMed=10585417;
RA Kline J.B., Roehrs H., Clevenger C.V.;
RT "Functional characterization of the intermediate isoform of the human
prolactin receptor."
RL J. Biol. Chem. 274:35461-35468 (1999).
DR HSSP; P16471; 1BP3.
DR EMBL; AF166329; AAD49655.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 288 AA; 32760 MW; B45203EC045EB417 CRC64;

Query Match 99.1%; Score 1155.5; DB 4; Length 288;
Best Local Similarity 99.5%; Pred. No. 7.2e-109;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60
Db 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNNAT-OMGSSFSDELYVD 119
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNNATQMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKEKAAEW 179
Db 121 VTYIVQDPDPLEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKEKAAEW 180
QY 180 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 210
Db 181 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 3
Q9UHJ5
ID Q9UHJ5 PRELIMINARY; PRT; 349 AA.

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AC Q9UHJ5;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Intermediate prolactin receptor isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20054419; PubMed=10585417;
RA Kline J.B., Roehrs H., Clevenger C.V.;
RT "Functional characterization of the intermediate isoform of the human
prolactin receptor."
RL J. Biol. Chem. 274:35461-35468 (1999).
DR HSSP; P16471; 1BP3.
DR EMBL; AF166329; AAD49655.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 349 AA; 39806 MW; 932F200E850CDD27 CRC64;

Query Match 99.1%; Score 1155.5; DB 4; Length 349;
Best Local Similarity 99.5%; Pred. No. 9.1e-109;
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60
Db 1 MKNVASATVFTLLFLNTCLLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNY 60
QY 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNNAT-OMGSSFSDELYVD 119
Db 61 SLTYHREGETLMHECPDYITGGPNSCHFGKQYTSWRTYIMVNNATQMGSSFSDELYVD 120
QY 120 VTYIVQDPDPLEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKEKAAEW 179
Db 121 VTYIVQDPDPLEAVEVQPEDRKPYLWKSPPTLIDLKTGWFTLLYEIRLKEKAAEW 180
QY 180 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 210
Db 181 EHFAGQOTEFKILSLHPGQKYLQVVRCKPD 211

RESULT 4
Q96P35
ID Q96P35 PRELIMINARY; PRT; 376 AA.
AC Q96P35;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DE Prolactin receptor short isoform B.
GN PRLR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Trott J.F., Hovey R.C., Vonderhaar B.K.;
RT "Expression of two novel hPRLR isoforms in breast tumors."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416619; AAL23915.1; -.
DR PIR; A59405; A59405.

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DR GO; GO:0016020; C.membrane; IEA.  
DR GO; GO:0004896; F.hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F.receptor activity; IEA.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor.  
SQ SEQUENCE 376 AA; 42639 MW; 112DC2555FBC4601 CRC64;  
  
Query Match 99.1%; Score 1155.5; DB 4; Length 376;  
Best Local Similarity 99.5%; Pred. No. 9.9e-109;  
Matches 210; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
  
QY 1 MKENVASATVFTLLFLNTCLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
Db 1 MKENVASATVFTLLFLNTCLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
  
QY 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVD 119  
Db 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVD 120  
  
QY 120 VTYIVQPPPLELAVEVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 179  
Db 121 VTYIVQPPPLELAVEVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 180  
  
QY 180 EIHFAQQQTEFKILSLHPGQKYLQVVRCKPD 210  
Db 181 EIHFAQQQTEFKILSLHPGQKYLQVVRCKPD 211  
  
RESULT 5  
Q865V4 PRELIMINARY; PRT; 622 AA.  
AC Q865V4;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Prolactin receptor long form.  
GN PRLR.  
OS Cebus apella (Brown-capped capuchin).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.  
OX NCBI\_TaxID=9515;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rojas-Garcia P.P., Germain A., Torres-Parfan C.L., Richter H.G.,  
RA Campino C., Seron-Ferre M.J.;  
RT "Expression of prolactin (PRL) receptor in ovary of capuchin monkey.  
RT Initial studies.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY227708; AAO73437.1; -.  
DR GO; GO:0016020; C.membrane; IEA.  
DR GO; GO:0004896; F.hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F.receptor activity; IEA.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor.  
SQ SEQUENCE 622 AA; 69597 MW; BF794773C1FCADB3 CRC64;  
  
Query Match 93.4%; Score 1088.5; DB 6; Length 622;  
Best Local Similarity 91.9%; Pred. No. 1.1e-101;  
Matches 194; Conservative 8; Mismatches 8; Indels 1; Gaps 1;  
  
QY 1 MKENVASATVFTLLFLNTCLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60

Db 1 MKENVASATVFTLLFLNTCLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
  
QY 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVD 119  
Db 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVD 120  
  
QY 120 VTYIVQPPPLELAVEVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 179  
Db 121 VTYIVQPPPLELAVEVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 180  
  
QY 180 EIHFAQQQTEFKILSLHPGQKYLQVVRCKPD 210  
Db 181 EIHFAQQQTEFKILSLHPGQKYLQVVRCKPD 211  
  
RESULT 6  
Q9NOJ7 PRELIMINARY; PRT; 622 AA.  
AC Q9NOJ7;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Prolactin receptor precursor.  
OS Callithrix jacchus (Common marmoset).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.  
OX NCBI\_TaxID=9483;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20457117; PubMed=11000523;  
RA Daltymple A., Edery M., Jabbour H.;  
RT "Sequence and functional characterization of the marmoset monkey  
RT (Callithrix jacchus) prolactin receptor: comparative homology with the  
RT human long-form prolactin receptor.";  
RL Mol. Cell. Endocrinol. 167:89-97 (2000).  
DR EMBL; AJ272217; CAB75847.1; -.  
DR HSSP; P16471; 1BP3.  
DR GO; GO:0016020; C.membrane; IEA.  
DR GO; GO:0004896; F.hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F.receptor activity; IEA.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR Pfam; PF00041; fn3; 2.  
DR SMART; SM00060; FN3; 2.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
KW Receptor; Signal.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 622 PROLACTIN RECEPTOR.  
SQ SEQUENCE 622 AA; 69425 MW; 65F99522C6CD6DB6 CRC64;  
  
Query Match 90.3%; Score 1052.5; DB 6; Length 622;  
Best Local Similarity 87.2%; Pred. No. 5.1e-98;  
Matches 184; Conservative 13; Mismatches 13; Indels 1; Gaps 1;  
  
QY 1 MKENVASATVFTLLFLNTCLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
Db 1 MKENVASATVFTLLFLNTCLNGQLPGKPEIFKCRSPNKETFTCWRRPGTGGGLPTNY 60  
  
QY 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVD 119  
Db 61 SLTYHREGETLMHECPDYITGPNCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVD 120  
  
QY 120 VTYIVQPPPLELAVEVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 179  
Db 121 VTYIVQPPPLELAVEVKQPEDKPYLWKSPPTLIDLTGWTLLYEIRLKPKEAAEW 180  
  
QY 180 EIHFAQQQTEFKILSLHPGQKYLQVVRCKPD 210  
Db 181 EIHFAQQQTEFKILSLHPGQKYLQVVRCKPD 211



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RESULT 7
ID Q16354 PRELIMINARY; PRT; 206 AA.
AC Q16354;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Prolactin receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95286597; PubMed=7768908;
RA Fuh G., Wells J.A.;
RT "Prolactin receptor antagonists that inhibit the growth of breast
RT cancer cell lines.";
RL J. Biol. Chem. 270:13133-13137(1995).
DR EMBL; S78505; AAB34470.1; -.
DR HSSP; P16471; 1BP3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
FT NON-TER.
SQ SEQUENCE 206 AA; 23950 MW; CED939781B3C804E CRC64;

Query Match 88.9%; Score 1036.5; DB 4; Length 206;
Best Local Similarity 99.5%; Pred. No. 5.6e-97;
Matches 186; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 25 QLPKGPETFKCRSPNKETFTCWEPGTDGGLPTNYSITVHREGTLMHPCPYITGGPN 84.
DB 1 QLPKGPETFKCRSPNKETFTCWEPGTDGGLPTNYSITVHREGTLMHPCPYITGGPN 60

QY 85 SCHFGKQYTMWRTYIMVNAT-QMGSSFSDELIVDTYIVQDPPLLEAVEVKQPEDRK 143
DB 61 SCHFGKQYTMWRTYIMVNATNQMGSSFSDELIVDTYIVQDPPLLEAVEVKQPEDRK 120

QY 144 PYLWIKWSPPTLIDLTGTFLLYRILKPKAAEWIHFAGQOTEFKILSLHPGOKYLV 203
DB 121 PYLWIKWSPPTLIDLTGTFLLYRILKPKAAEWIHFAGQOTEFKILSLHPGOKYLV 180

QY 204 QVRCKPD 210
DB 181 QVRCKPD 187

RESULT 8
Q9XS92 PRELIMINARY; PRT; 625 AA.
ID Q9XS92;
AC Q9XS92;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prolactin receptor precursor.
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
[1]
RP SEQUENCE FROM N.A.
RX TISSUE=Testis;
MEDLINE=99236966; PubMed=10221777;

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RA Demmer J.;
RT "The prolactin receptor from the brushtail possum (Trichosurus
RT vulpecula): CDNA cloning, expression and functional analysis.";
RL Mol. Cell. Endocrinol. 148:119-127(1999).
DR EMBL; AF098296; AAD27039.1; -.
DR HSSP; P16471; 1BP3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR008957; FN.III-like.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Signal.
FT SIGNAL 1 24 POTENTIAL
FT CHAIN 25 625 PROLACTIN RECEPTOR.
SQ SEQUENCE 625 AA; 70539 MW; 2097D72827C9DB86 CRC64;

Query Match 76.2%; Score 888.5; DB 6; Length 625;
Best Local Similarity 73.9%; Pred. No. 2.2e-81;
Matches 156; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

QY 1 MKNVAVATVPTLLFLNTCLANGQLPPGKPEIFKCRSPNKETFTCWEPGTDGGLPTNY 60
DB 1 MKNVTSATAPLFLLLFHTLLGQAGPKPKIEKCRSPKETFTCWWRPGSDGGIPTNY 60

QY 61 SLTYHREGTIMHECPDYITGGPNSCHFGKQYTMWRTYIMVNAT-QMGSSFSDELIVDT 119
DB 61 TLFYRKGESLTHCEPDYKGTGGPNSCVFNKKHTSIWVYIIWVNATNQMGSSFSDELIVDT 120

QY 120 VTYIVQDPPLLEAVEVKQPEDRKPYLWIKWSPPTLIDLTGTFLLYRILKPKAAEW 179
DB 121 VTYIVQDPPLLEAVEVKQPEDRKPYLWIKWSPPTLIDLTGTFLLYRILKPKAAEW 180

QY 180 EHFAGQOTEFKILSLHPGOKYLVQVRCKPD 210
DB 181 EHFAGQOTQKIFSLYLGGKYLVEVRCKPD 211

RESULT 9
Q8C7G1 PRELIMINARY; PRT; 292 AA.
ID Q8C7G1;
AC Q8C7G1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prolactin receptor related sequence 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK050317; BAC34185.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR008957; FN.III-like.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.

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SQ SEQUENCE 292 AA; 33618 MW; 9D60422B5E88A19 CRC64;
Query Match 69.9%; Score 814.5; DB 11; Length 292;
Best Local Similarity 69.8%; Pred. No. 2.8e-74;
Matches 143; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

QY 7 SATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLYTHR 66
DB 2 SSALAYNLLVLSISLLNGQSPGKPEIHKCRSPDKETFTCWWRPGSDGGLPTNYSLSYK 61
QY 67 EGETLMHECDPYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDYVIVQ 125
DB 62 EGEKNTVECDPYITGGPNSCFKQYTSWRTYIMVNATNGSGTSPLVDYVDYVIVE 121
QY 126 PDPLELAVVKQPEDEKPKYLWIKWSPPTLIDLTGFTLLYIRLKPKEAAEWEIHFAG 185
DB 122 PEPRNLTLVQKVKQKXTLWKLWLPPTITDVKTGFTMEYIRLKSDEADEWEIHFAG 181
QY 186 QTEFKLSLHPGQKYLQVRCRCPD 210
DB 182 HQTOFKVFDLYPGQKYLQVTRCRPD 206

RESULT 10
Q99JZ1 PRELIMINARY; PRT; 608 AA.
AC Q99JZ1;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Prolactin receptor.
GN PRLR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005555; AA05555.1; -.
DR EMBL; BC006652; AA06652.1; -.
DR HSSP; P16471; 1BP3.
DR MGB; MGI:97763; Prlr.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III-like.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor.
SQ SEQUENCE 608 AA; 68223 MW; 2710DAEC2B1A8F63 CRC64;

Query Match 69.6%; Score 811.5; DB 11; Length 608;
Best Local Similarity 71.4%; Pred. No. 1.4e-73;
Matches 142; Conservative 23; Mismatches 33; Indels 1; Gaps 1;

QY 13 LLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLYTHREGETLM 72
DB 8 MLLVLSISLLNGQSPGKPEIHKCRSPDKETFTCWWRPGSDGGLPTNYSLSYKEGKNT 67
QY 73 HECDPYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVDYVIVQDPDPLE 131
DB 68 YECDPYITGGPNSCFKQYTSWRTYIMVNATNGSGTSPLVDYVDYVIVEPDPN 127
QY 132 LAVEVKQPEDEKPKYLWIKWSPPTLIDLTGFTLLYIRLKPKEAAEWEIHFAGQTEFK 191
DB 128 LILEVKQLKDKXTLWKLWLPPTITDVKTGFTMEYIRLKSDEADEWEIHFAGTQFK 187
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QY 192 ILSLHPGQKYLQVRCRCPD 210
DB 188 VFDLYPGQKYLQVTRCRPD 206

RESULT 11
Q18985 PRELIMINARY; PRT; 198 AA.
AC Q18985;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Soluble prolactin receptor.
GN PROLACTIN RECEPTOR.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98389256; PubMed=9723863;
RA Jabbour H.N.; Clarke L.A.; Bramley T.; Postal-Vinay M.C.; Kelly P.A.;
RA Edery M.;
RT "Alternative splicing of the prolactin receptor gene generates a 1.7
RT kb RNA transcript that is linked to prolactin function in the red deer
RT testis."
RL J. Mol. Endocrinol. 21:51-59(1998).
DR EMBL; Y14753; CAA75048.1; -.
DR HSSP; P16471; 1BP3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III-like.
DR InterPro; IPR008957; FN_III-like.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 198 AA; 22652 MW; C020E070D970AC40 CRC64;

Query Match 65.6%; Score 764.5; DB 6; Length 198;
Best Local Similarity 72.9%; Pred. No. 2.1e-69;
Matches 132; Conservative 21; Mismatches 27; Indels 1; Gaps 1;

QY 1 MKENVASATVFTLLFLNTCLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNY 60
DB 1 MKENVASRAVFTLLFLNASLLNGQSPGKPKIIRCSFGKETFTCWWRPGSDGGLPTNY 60
QY 61 SLTYHREGETLMHECDPYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELYVD 119
DB 61 TLTTHKEGETLMHECDPYITGGPNTCYFSKHTSIWKIIVITVAINQNGVSSDPLYVD 120
QY 120 VTIVQDPDPLELAVVKQPEDEKPKYLWIKWSPPTLIDLTGFTLLYIRLKPKEAAEW 179
DB 121 VTIVVEPPANITLLEKHPEDRKPKYLWIKWFPPTLTDVKGWFMFIQYIRLKPETATDW 180
QY 180 E 180
DB 181 E 181

RESULT 12
Q8TD76 PRELIMINARY; PRT; 197 AA.
AC Q8TD76;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Delta 4-delta 7/11 truncated prolactin receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
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RP SEQUENCE FROM N.A.  
RC TISSUE=Breast tumor;  
RA Trott J.F., Hovey R.C., Koduri S., Vonderhaar B.K.;  
RT "Expression of multiple human prolactin receptor variants in breast  
and colon cancer derived by splicing to exon 11."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF493068; AAM11660.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; P:receptor activity; IEA.  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SMO0060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
DR KW Receptor.  
SQ SEQUENCE 197 AA; 22718 MW; D916BC915621EEEF CRC64;  
Query Match 65.1%; Score 759.5; DB 4; Length 197;  
Best Local Similarity 99.3%; Pred. No. 6.6e-69;  
Matches 139; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 72 MHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELVDVYIVQDPPL 130  
DB 1 MHECPDYITGGPNSCHFGKQYTSWRTYIMVNATQMGSSFSDELVDVYIVQDPPL 60  
QY 131 ELAVEVKQPEDRKPYLWIKWSPPTLIDLTGWTLLYEIRLKPKEAAEWEIHFGAQOTEF 190  
DB 61 ELAVEVKQPEDRKPYLWIKWSPPTLIDLTGWTLLYEIRLKPKEAAEWEIHFGAQOTEF 120  
QY 191 KILSLHPGQKYLQVRCRCPD 210  
DB 121 KILSLHPGQKYLQVRCRCPD 140  
QY 191 KILSLHPGQKYLQVRCRCPD 210  
DB 121 KILSLHPGQKYLQVRCRCPD 140  
RESULT 13  
Q8TD75 ID Q8TD75 PRELIMINARY; PRT; 217 AA.  
AC Q8TD75  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DE Delta 4-Sf1b truncated prolactin receptor.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast tumor;  
RA Trott J.F., Hovey R.C., Koduri S., Vonderhaar B.K.;  
RT "Expression of multiple human prolactin receptor variants in breast  
and colon cancer derived by splicing to exon 11."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF493068; AAM11660.1; -  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; P:receptor activity; IEA.  
DR InterPro; IPR003961; FN.III.  
DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SMO0060; FN3; 1.  
DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
DR KW Receptor.  
SQ SEQUENCE 217 AA; 24773 MW; E59A9BB9016C3397 CRC64;  
Query Match 65.1%; Score 759.5; DB 4; Length 217;  
Best Local Similarity 99.3%; Pred. No. 7.4e-69;  
Matches 139; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 72 MHECPDYITGGPNSCHFGKQYTSWRTYIMVNAT-QMGSSFSDELVDVYIVQDPPL 130  
DB 1 MHECPDYITGGPNSCHFGKQYTSWRTYIMVNATQMGSSFSDELVDVYIVQDPPL 60  
QY 191 KILSLHPGQKYLQVRCRCPD 210  
DB 121 KILSLHPGQKYLQVRCRCPD 140  
RESULT 14  
Q9GLW3 ID Q9GLW3 PRELIMINARY; PRT; 227 AA.  
AC Q9GLW3  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE Prolactin receptor (Fragment).  
OS Ursus maritimus (Polar bear) (Thalactos maritimus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
CX NCBI\_TaxID=29073;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20086658; PubMed=10618652;  
RA Howell-Skalla L.A., Bunick D., Bleck G.T., Nelson R.A., Bahr J.M.;  
RT "Cloning and sequence analysis of the extracellular region of the  
polar bear (Ursus maritimus) luteinizing hormone receptor (LHR),  
RT follicle stimulating hormone receptor (FSHR), and prolactin receptor  
RT (PRLr) genes and their expression in the testis of the black bear  
RT (Ursus americanus).";  
RL Mol. Reprod. Dev. 55:136-145(2000).  
DR EMBL; AF169792; AAG10648.1; -  
DR HSSP; Pf6471; IIP3.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN.III.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SMO0060; FN3; 1.  
DR Receptor.  
FT NON\_TER 1 227  
FT NON\_TER 227 227  
SQ SEQUENCE 227 AA; 26114 MW; F5E6C5F33B5D5849 CRC64;  
Query Match 65.1%; Score 758.5; DB 6; Length 227;  
Best Local Similarity 75.4%; Pred. No. 9.8e-69;  
Matches 129; Conservative 22; Mismatches 19; Indels 1; Gaps 1;  
QY 41 KETFTCWRRPGTGGTNYSLYTHREGETLMECPDYITGGPNSCHFGKQYTSWRTYI 100  
DB 1 KETFTCWRRPGTGGTNYSLYTHREGETLMECPDYITGGPNSCHFGKQYTSWRTYI 60  
QY 101 MYVNAT-QMGSSFSDELVDVYIVQDPPL-ELAVEVKQPEDRKPYLWIKWSPPTLIDLK 159  
DB 61 ITNATQMGSSFSDELVDVYIVQDPPL-ELAVEVKQPEDRKPYLWIKWSPPTLIDLK 120  
QY 160 TGMFTLLYEIRLKPKEAAEWEIHFGAQOTEFKILSLHPGQKYLQVRCRCPD 210  
DB 121 SGWLTLYEIRLKPKEATWETHFGAQOTQFKILSLHPGQKYLQVRCRCPD 171  
RESULT 15  
Q7T2Z0 ID Q7T2Z0 PRELIMINARY; PRT; 460 AA.  
AC Q7T2Z0  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DE Prolactin receptor (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

QY 131 ELAVEVKQPEDRKPYLWIKWSPPTLIDLTGWTLLYEIRLKPKEAAEWEIHFGAQOTEF 190  
DB 61 ELAVEVKQPEDRKPYLWIKWSPPTLIDLTGWTLLYEIRLKPKEAAEWEIHFGAQOTEF 120  
QY 191 KILSLHPGQKYLQVRCRCPD 210  
DB 121 KILSLHPGQKYLQVRCRCPD 140  
RESULT 14  
Q9GLW3 ID Q9GLW3 PRELIMINARY; PRT; 227 AA.  
AC Q9GLW3  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DE Prolactin receptor (Fragment).  
OS Ursus maritimus (Polar bear) (Thalactos maritimus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.  
CX NCBI\_TaxID=29073;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20086658; PubMed=10618652;  
RA Howell-Skalla L.A., Bunick D., Bleck G.T., Nelson R.A., Bahr J.M.;  
RT "Cloning and sequence analysis of the extracellular region of the  
polar bear (Ursus maritimus) luteinizing hormone receptor (LHR),  
RT follicle stimulating hormone receptor (FSHR), and prolactin receptor  
RT (PRLr) genes and their expression in the testis of the black bear  
RT (Ursus americanus).";  
RL Mol. Reprod. Dev. 55:136-145(2000).  
DR EMBL; AF169792; AAG10648.1; -  
DR HSSP; Pf6471; IIP3.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR002996; CRIA.  
DR InterPro; IPR003961; FN.III.  
DR Pfam; PF00041; fn3; 1.  
DR SMART; SMO0060; FN3; 1.  
DR Receptor.  
FT NON\_TER 1 227  
FT NON\_TER 227 227  
SQ SEQUENCE 227 AA; 26114 MW; F5E6C5F33B5D5849 CRC64;  
Query Match 65.1%; Score 758.5; DB 6; Length 227;  
Best Local Similarity 75.4%; Pred. No. 9.8e-69;  
Matches 129; Conservative 22; Mismatches 19; Indels 1; Gaps 1;  
QY 41 KETFTCWRRPGTGGTNYSLYTHREGETLMECPDYITGGPNSCHFGKQYTSWRTYI 100  
DB 1 KETFTCWRRPGTGGTNYSLYTHREGETLMECPDYITGGPNSCHFGKQYTSWRTYI 60  
QY 101 MYVNAT-QMGSSFSDELVDVYIVQDPPL-ELAVEVKQPEDRKPYLWIKWSPPTLIDLK 159  
DB 61 ITNATQMGSSFSDELVDVYIVQDPPL-ELAVEVKQPEDRKPYLWIKWSPPTLIDLK 120  
QY 160 TGMFTLLYEIRLKPKEAAEWEIHFGAQOTEFKILSLHPGQKYLQVRCRCPD 210  
DB 121 SGWLTLYEIRLKPKEATWETHFGAQOTQFKILSLHPGQKYLQVRCRCPD 171  
RESULT 15  
Q7T2Z0 ID Q7T2Z0 PRELIMINARY; PRT; 460 AA.  
AC Q7T2Z0  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DE Prolactin receptor (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

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OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Hui A.M.Y., Leung F.C.;
RT "Genomic characterization of chicken prolactin receptor gene.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY237376; AAP49452.1; -.
KW Receptor.
FT NON_CODING 460 460
SQ SEQUENCE 460 AA; 52901 MW; 947DA92892A19361 CRC64;

Query Match 59.3%; Score 691.5; DB 13; Length 460;
Best Local Similarity 62.4%; Pred. No. 1.4e-61;
Matches 118; Conservative 31; Mismatches 39; Indels 1; Gaps 1;

Qy 23 NGQLPRGKPEIFKCRSPKNETFTCWWRPGTDGGLPTNYSILYHREGETLMHECPDYITGG 82
Db 226 SGQSPPEKPTIHKRSPEKETFTCWWRKPGLDGGHPNYILLYSREGEEQVYECPDYETAG 285

Qy 83 PNSCHFQKQVTSMMRTYIMVNAT-QMGSSFSDELXVDVTYIVQDPDPLEAVEVKQPED 141
Db 286 PNSCYFDKHTSFTIYNITVRATNENGSSSDPHYVDVTYIVQDPDPPVAVTLELKKPIN 345

Qy 142 RKPVLTKWSPPTLIDLTGFWLLYHRLKPKAAWEIHFAGQOTEKILSLHSGQKY 201
Db 346 RKPVLVLTWSPPLADVRSGLTLEYELRKPEEGEWEETIFVGQOTQYKMFSLNPGKKY 405

Qy 202 LVQVRCKPD 210
Db 406 IIQHCKPD 414
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